

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 08:22:14 ; Search time 275 Seconds  
(without alignments)  
5371.468 Million cell updates/sec

Title: US-10-658-482-1  
Perfect score: 831  
Sequence: 1 cgtcctatctgcagtcggt.....caaccagagcattcttcgg 831

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*

- 1: /cgn2\_6/prodata/1/ina/1\_COMB.seq.\*
- 2: /cgn2\_6/prodata/1/ina/5\_COMB.seq.\*
- 3: /cgn2\_6/prodata/1/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/prodata/1/ina/H\_COMB.seq.\*
- 6: /cgn2\_6/prodata/1/ina/PCTUS\_COMB.seq.\*
- 7: /cgn2\_6/prodata/1/ina/PP\_COMB.seq.\*
- 8: /cgn2\_6/prodata/1/ina/RE\_COMB.seq.\*
- 9: /cgn2\_6/prodata/1/ina/backfileseq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	42.4	5.1	9007	3	Sequence 908, App
c 2	38	4.6	364	3	Sequence 17202, A
c 3	36.8	4.4	1335	3	Sequence 5256, App
c 4	36.8	4.4	34316	3	Sequence 1257, App
c 5	36	4.3	923	3	Sequence 69, Appl
c 6	35.8	4.3	1038	3	Sequence 3643, App
c 7	35.8	4.3	19269	3	Sequence 1175, App
c 8	35.8	4.3	26729	3	Sequence 6, Appl
c 9	35.8	4.3	70383	3	Sequence 13, Appl
c 10	35.4	4.3	3153	3	Sequence 15639, A
c 11	35.2	4.2	505	3	Sequence 53, Appl
c 12	35	4.2	589	3	Sequence 45047, A
c 13	35	4.2	601	3	Sequence 94, Appl
c 14	35	4.2	2662	3	Sequence 59, Appl
c 15	35	4.2	2662	3	Sequence 54, Appl
c 16	35	4.2	5275	3	Sequence 7038, App
c 17	34.8	4.2	825	3	Sequence 5, Appl
c 18	34.8	4.2	4152	3	Sequence 5, Appl
c 19	34.8	4.2	4152	3	Sequence 5, Appl
c 20	34.8	4.2	4152	3	Sequence 5, Appl
c 21	34.8	4.2	4152	3	Sequence 5, Appl
c 22	34.8	4.2	5570	3	Sequence 623, App
c 23	34.6	4.2	2040	3	Sequence 10, Appl
c 24	34.4	4.1	1123	3	Sequence 223, App

25	34.4	4.1	1123	3	US-09-902-540-6000	Sequence 6000, Ap
c 26	34.2	4.1	9408	3	US-09-949-016-13867	Sequence 13867, A
c 27	34.2	4.1	13187	3	US-09-422-936-61	Sequence 61, Appl
c 28	34.2	4.1	127280	3	US-09-949-016-14857	Sequence 14857, A
c 29	34.2	4.1	132266	3	US-09-949-016-14860	Sequence 14860, A
c 30	34.2	4.1	150833	3	US-09-949-016-14859	Sequence 14859, A
c 31	34.2	4.1	159963	3	US-09-949-016-14858	Sequence 14858, A
c 32	34.2	4.1	171130	3	US-09-949-016-14861	Sequence 14861, A
c 33	34.2	4.1	784019	3	US-09-949-016-14033	Sequence 14033, A
c 34	34.2	4.1	828152	3	US-09-949-016-12777	Sequence 12777, A
c 35	33.8	4.1	601	3	US-09-949-016-32733	Sequence 32733, A
c 36	33.8	4.1	601	3	US-09-949-016-32734	Sequence 32734, A
c 37	33.8	4.1	601	3	US-09-949-016-45044	Sequence 45044, A
c 38	33.8	4.1	601	3	US-09-949-016-45048	Sequence 45048, A
c 39	33.8	4.1	601	3	US-09-949-016-140295	Sequence 140295, A
c 40	33.8	4.1	601	3	US-09-949-016-140296	Sequence 140296, A
c 41	33.8	4.1	601	3	US-09-949-016-140297	Sequence 140297, A
c 42	33.8	4.1	601	3	US-09-949-016-142346	Sequence 142346, A
c 43	33.8	4.1	601	3	US-09-949-016-142347	Sequence 142347, A
c 44	33.8	4.1	1558	3	US-09-949-016-764	Sequence 764, App
c 45	33.8	4.1	1558	3	US-09-949-016-4025	Sequence 4025, Ap

#### ALIGNMENTS

##### RESULT 1

US-09-902-540-908/c  
; Sequence 908, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 908  
; LENGTH: 9007  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-908

Query Match	5.1%	Score 42.4;	DB 3;	Length 9007;
Best Local Similarity	58.9%	Pred. No. 0.058;		
Matches	73;	Conservative	0;	Mismatches 51;
			Indels	0;
			Gaps	0;
QY	330	TGCCCCCAGGTCGGCCCTGCGCTGACCTCCAGTCGCTGACCGTGAACGATACAGGGG	389	
Db	7069	TGTCACGCGCCCTGCTGCGCGTACCTGCTGACGCTGACCCCGACACGACGTGC	7010	
QY	390	AGTACTTCTGCACTATCACAACCTACCTGATGGACGCTGACACTGGGAGAACTTCTCTGG	449	
Db	7009	TGTCGCTGTCATGCACCATCATCTCGGACGCTGGTCCATGGGCGTCTGTCCTCGG	6950	
QY	450	AGGT 453		
Db	6949	AAAT 6946		

##### RESULT 2

US-09-621-976-17202  
; Sequence 17202, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.



GenCore version 5.1.7  
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 OM nucleic - nucleic search, using sw model  
 Run on: March 5, 2006, 20:46:53 ; Search time 4262 Seconds  
 (without alignments)  
 11083.273 Million cell updates/sec

Title: US-10-658-482-1  
 Perfect score: 831  
 Sequence: 1 cgtctatctcagtcggct.....caaccagagcattcttcgg 831

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : GenEmbl.\*

1: gb\_ba:\*  
 2: gb\_in:\*  
 3: gb\_env:\*  
 4: gb\_om:\*  
 5: gb\_ov:\*  
 6: gb\_pat:\*  
 7: gb\_ph:\*  
 8: gb\_pr:\*  
 9: gb\_ro:\*  
 10: gb\_sts:\*  
 11: gb\_sv:\*  
 12: gb\_un:\*  
 13: gb\_vi:\*  
 14: gb\_htg:\*  
 15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	818.4	98.5	1332	6	BD260690 50 human
2	788	94.8	1446	8	BC101290 Homo sapi
3	788	94.8	1448	8	BC101289 Homo sapi
4	788	94.8	1452	8	BC101291 Homo sapi
5	786.4	94.6	1448	8	BC101288 Homo sapi
6	785.8	94.6	2139	6	AX834616 Sequence
7	785.8	94.6	2139	8	AK097192 Homo sapi
8	670	80.6	2893	8	BX640915 Homo sapi
9	344	41.4	344	6	CQ717323 Sequence
10	333.6	40.1	131161	14	AC068938 Homo sapi
11	333.6	40.1	14213	14	AC073407 Homo sapi
12	333.6	40.1	151535	14	AC084188 Homo sapi
13	333.6	40.1	161077	8	AC093010 Homo sapi
14	333.6	40.1	181988	14	AC090552 Homo sapi
15	333.6	40.1	196832	14	AC027054 Homo sapi
16	333.6	40.1	318586	14	AC107422 Homo sapi
17	282	33.9	297	6	AX119215 Sequence
18	259	31.2	131161	14	AC068938 Homo sapi

19	259	31.2	318586	14	AC107422	AC107422 Homo sapi
20	234.6	28.2	220524	14	AC103065	AC103065 Rattus no
21	234.6	28.2	248938	14	AC095006	AC095006 Rattus no
c 22	234.6	28.2	253874	14	AC131560	AC131560 Rattus no
c 23	234.6	28.2	274703	14	AC110414	AC110414 Rattus no
24	233.6	28.1	158312	9	AC154408	AC154408 Mus muscu
25	184.6	22.2	70384	14	AC103977	AC103977 Homo sapi
26	149.2	18.0	157	6	CQ454533	CQ454533 Sequence
c 27	139.8	16.8	151535	14	AC084188	AC084188 Homo sapi
28	128	15.4	218995	9	AC120871	AC120871 Mus muscu
29	79	9.5	294	10	AB143947	AB143947 Homo sapi
30	77.2	9.3	207095	14	AC136844	AC136844 Rattus no
31	45.4	5.5	125020	8	AF429315	AF429315 Homo sapi
c 32	43	5.2	125020	8	AF429315	AF429315 Homo sapi
c 33	42.4	5.1	9007	6	AR619513	AR619513 Sequence
c 34	40.6	4.9	300242	1	AE016790	AE016790 Pseudomon
c 35	40.2	4.8	177661	9	AC119237	AC119237 Mus muscu
c 36	40.2	4.8	195768	8	AC022034	AC022034 Homo sapi
c 37	40.2	4.8	205744	14	AC162176	AC162176 Mus muscu
c 38	40	4.8	2000	6	AX655393	AX655393 Sequence
c 39	39.8	4.8	205893	14	AC115530	AC115530 Rattus no
c 40	39.8	4.8	293757	9	AC095491	AC095491 Rattus no
41	39.6	4.8	410	8	HSATIH114	X69545 H.sapiens g
c 42	39.4	4.7	169989	8	AC090137	AC090137 Homo sapi
c 43	39.4	4.7	174345	14	AC025236	AC025236 Homo sapi
c 44	39.4	4.7	174646	14	AC087355	AC087355 Homo sapi
c 45	39.4	4.7	181727	14	AC036232	AC036232 Homo sapi

#### ALIGNMENTS

RESULT 1	BD260690	1332 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD260690	50 human secreted proteins.			
DEFINITION	BD260690	50 human secreted proteins.			
ACCESSION	BD260690.1	GI:33070460			
VERSION	JP 2002539814-A/32.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 1332)				
AUTHORS	Rosen, C.A., Ruben, S.M. and Komatsoulis, G.				
TITLE	50 human secreted proteins				
JOURNAL	Patent: JP 2002539814-A 32 26-NOV-2002;				
COMMENT	HUMAN GENOME SCIENCES INC				
	OS Homo sapiens (human)				
	PN JP 2002539814-A/32				
	PD 26-NOV-2002				
	PF 22-MAR-2000 JP 2000608034				
	PR 26-MAR-1999 US 60/126594, 17-DEC-1999 US 60/172408 PI				
	CRAIG A ROSEN, STEVEN M RUBEN, GEORGE KOMATSOUIS PC				
	C12N15/09, A61K38/00, A61K48/00, A61P1/00, A61P1/04, A61P3/10 PC				
	, A61P7/02, A61P7/04,				
	PC A61P7/06, A61P7/08, A61P9/10, A61P11/00, A61P11/06, A61P13/12, PC				
	A61P17/02				
	PC A61P19/02, A61P21/04, A61P25/00, A61P25/28, A61P27/02, A61P29/00,				
	PC A61P29/00,				
	PC A61P31/18, A61P35/00, A61P37/00, A61P37/08, C07K14/47, C07K16/18,				
	PC C12N1/15,				
	PC C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12Q1/02, C12Q1/68, G01N33/				
	PC 53,				
	PC G01N33/56, G01N33/68, C12N15/00, A61K37/02, C12N5/00 CC 50				
	human secreted proteins				
	Key Location/Qualifiers				
	FT source 1. .1332				
	FT Location/Qualifiers				
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	/organism='Homo sapiens (human)'				
	source				
	/organism='Homo sapiens'				

/mol_type="genomic DNA"		/db_xref="taxon:9606"	
ORIGIN	Query Match	98.5%; Score 818.4; DB 6; Length 1332;	
	Best Local Similarity	99.8%; Pred. No. 2.6e-214; Mismatches 0; Indels 1; Gaps 1;	
	Matches 830; Conservative	0; Indels 1; Gaps 1;	
QY	1	CGTCTATCTGCAGTGGCTACTTTTCAGT-GGCAGAGAGGCCACATCTGCTTCTCTAG	59
DB	235	CGTCTATCTGCAGTGGCTACTTTTCAGTGGCAGAGAGGCCACATCTGCTTCTCTAG	294
QY	60	GCCTCTGGCAGAGCATGCGCTGCTCTCTCTGATCTGGCCCGAGGGGTGAGGC	119
DB	295	GCCTCTGGCAGAGCATGCGCTGCTCTCTCTGATCTGGCCCGAGGGGTGAGGC	354
QY	120	AGGCTCCCTCGCTCAGGATGATGACAGGCACATAGAAACACCGGGACATTTCTG	179
DB	355	AGGCTCCCTCGCTCAGGATGATGACAGGCACATAGAAACACCGGGACATTTCTG	414
QY	180	CAGAGAAAGGTGGCTCTATCTTACATGTACATGTCACTCTCTCCACACGCGCAAGTGA	239
DB	415	CAGAGAAAGGTGGCTCTATCTTACATGTCACTCTCTCCACACGCGCAAGTGA	474
QY	240	CCAGGTCAACTGGAGCAGCAGGACCAAGCTTCTGGCCATTTGTAATGTGACTTGGGT	299
DB	475	CCAGGTCAACTGGAGCAGCAGGACCAAGCTTCTGGCCATTTGTAATGTGACTTGGGT	534
QY	300	GGCACATCTCCCATCTTCAAGGATCAGTGGGCCCGAGGTCCTGGGCTGACCC	359
DB	535	GGCACATCTCCCATCTTCAAGGATCAGTGGGCCCGAGGTCCTGGGCTGACCC	594
QY	360	TCAGTGCCTGACCTGACGATACAGGGAGTACTTCTGCTATCTATCACACCTTACCC	419
DB	595	TCAGTGCCTGACCTGACGATACAGGGAGTACTTCTGCTATCTATCACACCTTACCC	654
QY	420	ATGGGACGTACACTGGGAGATCTTCTCGAGGTCCTAGAAAGCTCAGTGGCTGAGCAG	479
DB	655	ATGGGACGTACACTGGGAGATCTTCTCGAGGTCCTAGAAAGCTCAGTGGCTGAGCAG	714
QY	480	GTGCCAGGTTCCAGATTCATTTGTTGAGGATGCGCGAGCTGGTGGTCACTGCA	539
DB	715	GTGCCAGGTTCCAGATTCATTTGTTGAGGATGCGCGAGCTGGTGGTCACTGCA	774
QY	540	CAGCAGTCACTGTGTGTGCTGAGTCTAGAAAGAGAGAGCCCTCAGATCCATTTCTG	599
DB	775	CAGCAGTCACTGTGTGTGCTGAGTCTAGAAAGAGAGAGCCCTCAGATCCATTTCTG	834
QY	600	TGGAAGGTGACCTCAGGAGAAATCAGCTGGACAGGAGAAATGGAGGCCAGTCTCCCT	659
DB	835	TGGAAGGTGACCTCAGGAGAAATCAGCTGGACAGGAGAAATGGAGGCCAGTCTCCCT	894
QY	660	CACCCCCAGGAAGCTGTGTCAGGAGAGCTGCACTGTGGGCTCTGTGGAGAGCAGC	719
DB	895	CACCCCCAGGAAGCTGTGTCAGGAGAGCTGCACTGTGGGCTCTGTGGAGAGCAGC	954
QY	720	GGGAGAGGACTGTGCGGAGCTGATGACTTCAATGCTCCTGAGTTACAGAGCCTGG	779
DB	955	GGGAGAGGACTGTGCGGAGCTGATGACTTCAATGCTCCTGAGTTACAGAGCCTGG	1014
QY	780	GTAACGTGAGCTTCTTTCAGAGACTGGTTAGCAACACAGAGGCATCTTCTGG	831
DB	1015	GTAACGTGAGCTTCTTTCAGAGACTGGTTAGCAACACAGAGGCATCTTCTGG	1066
RESULT 2	BC101290	1446 bp	mRNA
LOCUS	BC101290		
DEFINITION	Homo sapiens hypothetical protein FLJ39873, mRNA (cDNA clone		
ACCESSION	MGC:120351 IMAGE:40024496), complete cds.		
VERSION	BC101290		
KEYWORDS	BC101290.1 GI:71680560		
	MGC.		

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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 20:40:23 ; Search time 476 Seconds  
(without alignments)  
11635.209 Million cell updates/sec

Title: US-10-658-482-1

Perfect score: 831

Sequence: 1 cgtctattcgcagtcgct.....caaccagagcgcatctctcgg 831

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

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- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	831	100.0	831	12	ADM32155
2	831	100.0	1711	9	ADM32155 PROS2254
3	818.4	98.5	1332	3	ADA21190 Human sec
4	818.4	98.5	1332	3	AAC95484 Human sec
5	796	95.8	860	10	ADL91491 Human imm
6	785.8	94.6	2139	11	ADL76824 Novel hum
7	775.8	93.4	1500	10	ADM03055 Human cDN
8	775.8	93.4	1500	10	ADM07073 Novel cod
9	696.8	83.9	1164	10	ADU40230 Novel hum
10	414.8	49.9	1006	12	ADL08854 Novel DNA
11	282	33.9	297	5	ADM32157 Mouse PRO
12	149.2	18.0	157	6	Aah52282 Human AFP
13	42.4	5.1	9007	14	ABN25908 Human ORF
14	40.6	4.9	1590	8	ACL64445 M. xanthu
15	40	4.8	2000	8	ACA43911 Prokaryot
16	39.2	4.7	2000	8	ADA71938 Rice gene
17	36.8	4.4	1335	14	ADA71938 Rice gene
18	36.8	4.4	34316	14	ACL68793 M. xanthu
19	36	4.3	993	2	ACL64794 M. xanthu
					Aax86266 DNA encod

20	36	4.3	993	6	ABL68586	Ab168586 Kidney ca
21	36	4.3	993	12	ABN97448	Abn97448 Gene #394
22	36	4.3	993	12	ADQ18253	Adq18253 Human gof
23	36	4.3	993	13	ADS64464	Ads64464 Human gof
24	35.8	4.3	1038	14	ACL67180	Ac167180 M. xanthu
25	35.8	4.3	19269	14	ACL64712	Ac164712 M. xanthu
26	35.8	4.3	26729	9	AA160439	Aa160439 Human kin
27	35.8	4.3	70383	9	AA160437	Aa160437 Human kin
28	35.4	4.3	1434	13	ADX53235	Adx53235 Plant ful
29	35.4	4.3	3153	6	ABK10187	Abk10187 Tkr/tdnd/
30	35.2	4.2	591	5	AAS80984	Aas80984 DNA encod
31	35.2	4.2	837	5	ABZ51888	Abz51888 Aspergill
32	35.2	4.2	1051	13	ADX54131	Adx54131 Plant ful
33	35.2	4.2	1060	13	ADX47445	Adx47445 Plant ful
34	35.2	4.2	3397	13	ADR83464	Adr83464 Human TEF
35	35	4.2	569	4	AAF29686	Aaf29686 P acnes 1
36	35	4.2	1375	3	AAC76701	Aac76701 Human ORF
37	35	4.2	1441	4	AAI61227	Aai61227 Human pol
38	35	4.2	1610	4	AA105775	Aa105775 Human rep
39	35	4.2	1917	6	ABK51101	Abk51101 cDNA enco
40	35	4.2	1991	5	AAC88096	Aac88096 Human FLE
41	35	4.2	2000	6	ABQ60910	Abq60910 Clone IMA
42	35	4.2	2436	4	AAH17901	Aah17901 Human cDN
43	35	4.2	2646	13	ACN39005	Acn39005 Tumour-as
44	35	4.2	2662	8	ABX70867	Abx70867 Novel hum
45	35	4.2	2849	13	ADT43085	Adt43085 Bacterial

#### ALIGNMENTS

#### RESULT 1

ADM32155  
ID ADM32155 standard; cDNA; 831 BP.

XX ADM32155;

XX 17-JUN-2004 (first entry)

XX PROS2254 cDNA, seq id 1.

XX Immunosuppressive; dermatological; hepatotropic; nephrotropic;  
XX antidiabetic; antiaslatic; antipsoriatic; antiallergic; antianaemic;  
XX antiarteriosclerotic; antiarthritic; neuroprotective; respiratory;  
XX antiinflammatory; gene therapy; rheumatoid arthritis; asthma; gene; ss.

XX Unidentified.

XX Key Location/Qualifiers  
XX CDS 77..811  
XX FT /\*tag= a  
XX FT /product= "PROS2254"

XX WO2004024068-A2.

XX PD 25-MAR-2004.

XX PF 09-SEP-2003; 2003WO-US028202.

XX PR 11-SEP-2002; 2002US-0410062P.

XX (GETH ) GENENTECH INC.

XX PI Baldwin DT, Bodary SC, Chan AC, Clark H, Jackman JK, Wood WT;

XX DR WPI; 2004-269871/25.

XX DR P-PSDB; ADM32156.

XX PT New PROS2254 nucleic acid or polypeptide, useful for preparing a  
XX composition for diagnosing or treating in a mammal an immune related  
XX disorder e.g. systemic lupus erythematosus.

XX PS Claim 3; SEQ ID NO 1; 100pp; English.

XX	CC	The invention relates to an isolated PRO52254 nucleic acid. Further
CC	CC	disclosed is a vector comprising the nucleic acid. The PRO52254 nucleic
CC	CC	acid or polypeptide is useful for preparing a composition for diagnosing
CC	CC	or treating an immune related disorder, e.g., systemic lupus
CC	CC	erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic
CC	CC	arthritis, spondyloarthritis, systemic sclerosis, idiopathic
CC	CC	inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,
CC	CC	sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia,
CC	CC	thyroiditis, diabetes mellitus, immune-mediated renal disease, a
CC	CC	demyelinating disease of the central or peripheral nervous system,
CC	CC	idiopathic demyelinating polyneuropathy, Guillain-Barr syndrome, chronic
CC	CC	inflammatory demyelinating polyneuropathy, hepatobiliary disease,
CC	CC	infectious or autoimmune chronic active hepatitis, primary biliary
CC	CC	cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory
CC	CC	bowel disease, gluten-sensitive enteropathy, Whipple's disease,
CC	CC	autoimmune or immune-mediated skin disease, bullous skin disease,
CC	CC	erythema multiforme, contact dermatitis, psoriasis, allergic disease,
CC	CC	asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity,
CC	CC	urticaria, immunologic disease of the lung, eosinophilic pneumonias,
CC	CC	idiopathic pulmonary fibrosis, hypersensitivity pneumonitis,
CC	CC	transplantation associated disease, graft rejection or graft-versus-host-
CC	CC	disease. The current sequence represents the PRO52254 nucleotide
CC	CC	sequence.
XX	CC	
QQ	CC	Sequence 831 BP; 186 A; 234 C; 238 G; 173 T; 0 U; 0 Other;
	CC	Query Match 100.0%; Score 831; DB 12; Length 831;
	CC	Best Local Similarity 100.0%; Pred. No. 4.6e-226;
	CC	Matches 831; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1	CGTCCTATCTGCAGTCGGCTACTTTTCAGTGGCAGAGGCCACATCTGCTCTCTGTAGG 60
DB	1	CGTCCTATCTGCAGTCGGCTACTTTTCAGTGGCAGAGGCCACATCTGCTCTCTGTAGG 60
QY	61	CCCTCTGGCAGAGCATCGTGTCCTCTCTGATCTGGGCCCAGGGGCTGAGGCA 120
DB	61	CCCTCTGGCAGAGCATCGTGTCCTCTCTGATCTGGGCCCAGGGGCTGAGGCA 120
QY	121	GGCTCCCTCGCTCAGGAATCATCAGGCACATAGAAACACGGGGAACTTCTGC 180
DB	121	GGCTCCCTCGCTCAGGAATCATCAGGCACATAGAAACACGGGGAACTTCTGC 180
QY	181	AGAGAAAGTGGCTCTATCATCTTACAATGTCACTCTCTCCACACGGCACAAGTGAC 240
DB	181	AGAGAAAGTGGCTCTATCATCTTACAATGTCACTCTCTCCACACGGCACAAGTGAC 240
QY	241	CCAGGTCAACTGGAGCAGCAGGACCACTTCTGGCCATTTGTAACTGCTATGGGGTG 300
DB	241	CCAGGTCAACTGGAGCAGCAGGACCACTTCTGGCCATTTGTAACTGCTATGGGGTG 300
QY	301	GCACATCTCCCATCTTCAAGGATCGAGTGGCCCCAGGTCCCGGCTGGGGCTCACCT 360
DB	301	GCACATCTCCCATCTTCAAGGATCGAGTGGCCCCAGGTCCCGGCTGGGGCTCACCT 360
QY	361	CCAGTCGCTGACCGTGAAAGTACAGGGGAGTACTTCTGCATCTATCACACTACCTGA 420
DB	361	CCAGTCGCTGACCGTGAAAGTACAGGGGAGTACTTCTGCATCTATCACACTACCTGA 420
QY	421	TGGGACGTACACTGGGAGGAATCTTCTCGAGAGTCTCTAGAAAGCTCAGTGGCTGAGCAGG 480
DB	421	TGGGACGTACACTGGGAGGAATCTTCTCGAGAGTCTCTAGAAAGCTCAGTGGCTGAGCAGG 480
QY	481	TGCAGGTTCCAGATTCCTATTCGTTGGAGCCATATGGCCGCGACGCTGGTGGTCACTTGCAC 540
DB	481	TGCAGGTTCCAGATTCCTATTCGTTGGAGCCATATGGCCGCGACGCTGGTGGTCACTTGCAC 540
QY	541	AGCAGTCACTGTTGGTTCGCTGACTAGAAAGAAAGAACCCCTCAGAAATCCATTCTGT 600
DB	541	AGCAGTCACTGTTGGTTCGCTGACTAGAAAGAAAGAACCCCTCAGAAATCCATTCTGT 600
QY	601	GGAGGTGCCTCAGGAGAAAATACAGCTGGACAGGAGGAATTGGAGCCCCAGTGTCTCCCTC 660

Db	601	GGAAAGTGACCTCAGAGAAATCAGCTGCACAGGAGGAGTGGAGCCCCAGTGTCTCCCTC	660
Qy	661	ACCCCCAGGAAGCTGTGTCCAGGCAGAGCTGCACCTGTCTGGGCTCTGTGGAGAGCAGCG	720
Db	661	ACCCCCAGGAAGCTGTGTCCAGGCAGAGCTGCACCTGTCTGGGCTCTGTGGAGAGCAGCG	720
Qy	721	GGGAGGAGCTGTCCGAGCTGCATGACTACTTCAATGTCTCTGAGTTACAGAGCCTGGG	780
Db	721	GGGAGGAGCTGTCCGAGCTGCATGACTACTTCAATGTCTCTGAGTTACAGAGCCTGGG	780
Qy	781	TAACTGCAGCTTCTTTCACACAGACTGGTTAGCAACACAGAGGCATCTTCTGG	831
Db	781	TAACTGCAGCTTCTTTCACACAGACTGGTTAGCAACACAGAGGCATCTTCTGG	831
RESULT 2			
ADA21190			
ID	ADA21190	standard; cDNA; 1711 BP.	
XX	AC		
XX	AC		
XX	AC		
XX	AC		
DT	20-NOV-2003	(first entry)	
XX			
DE		Human secreted protein SECP-44 encoding cDNA SEQ ID NO:95.	
XX			
KW		human; secreted protein; SECP; anti-HIV; anti-allergic; anti-inflammatory;	
KW		antianaemic; antiparkinsonian; nontropic; anticonvulsant;	
KW		antiarteriosclerotic; antiasthmatic; immunosuppressive; antithyroid;	
KW		cytostatic; hepatotropic; dermatological; antidiabetic; nephrotropic;	
KW		antigout; thyromimetic; neuroprotective; osteopathic; antiarthritic;	
KW		antiparasitic; antihelminthic; antipsoriatic; uropathic;	
KW		ophthalmological; antirheumatic; haemostatic; antibacterial; virucide;	
KW		protease; fungicide; gene therapy; cell proliferative disorder;	
KW		arteriosclerosis; atherosclerosis; cirrhosis; hepatitis;	
KW		paroxysmal nocturnal haemoglobinuria; polycythaemia vera; psoriasis;	
KW		primary thrombocytopaenia; cancer; developmental disorder;	
KW		renal tubular acidosis; anaemia; mental retardation;	
KW		neurological disorder; Alzheimer's disease; Parkinson's disease;	
KW		epilepsy; autoimmune disorder; inflammatory disorder; AIDS; allergy;	
KW		asthma; autoimmune thyroiditis; contact dermatitis; Crohn's disease;	
KW		diabetes mellitus; glomerulonephritis; Goodpasture's syndrome; gout;	
KW		Graves' disease; Hashimoto's thyroiditis; irritable bowel syndrome;	
KW		multiple sclerosis; osteoarthritis; osteoporosis; pancreatitis;	
KW		Reiter's syndrome; rheumatoid arthritis; Sjogren's syndrome; uveitis;	
KW		infection; gene; ss.	
XX			
OS		Homo sapiens.	
XX			
FN	WO2003068943-A2.		
XX			
PD	21-AUG-2003.		
XX			
PF	13-FEB-2003; 2003WO-US004712.		
XX			
PR	13-FEB-2002; 2002US-0357002P.		
PR	06-MAR-2002; 2002US-0362439P.		
PR	19-MAR-2002; 2002US-0366041P.		
XX			
PA	(INCY-) INCYTE GENOMICS INC.		
XX			
PI	Lehr-Mason PM, Kable AB, Elliott VS, Marquis JP, Baughn MR;		
PI	Chawla NK, Tran UK, Jin P, Tang YT, Zebariadian Y, Swarnakar A;		
PI	Hafalia AJA, Cocks BG, Warren BA, Emerling BM, Pearson CI, Chien D;		
PI	Peterson DP, Fu GK, Yue H, Jackson AA, Jiang X, Hawkins PR, Lal PG;		
PI	Khare R, Lee S, Lee SY, Richardson TW, Chang H;		
XX			
DR	WPI; 2003-689669/65.		
DR	P-PSDB; ADA21139.		
XX			
PT	New human secreted proteins and polynucleotides, useful for diagnosing,		
PT	treating or preventing autoimmune or inflammatory disorders (e.g. AIDS,		
PT	allergy, asthma or anaemia), multiple sclerosis, osteoporosis, cancer or		
PT	hepatitis.		

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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 20:49:07 ; Search time 3728 Seconds  
(without alignments)  
10429.202 Million cell updates/sec

Title: US-10-658-482-1

Perfect score: 831

Sequence: 1 cgtctatctgcagtcgctc.....caaccagaggaatctctcgg 831

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_est3:\*

4: gb\_hic:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_est7:\*

9: gb\_gss1:\*

10: gb\_gss2:\*

11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	831	100.0	3809	4	HS804486	AL833175 Homo sapi
2	763	91.8	763	11	DQ045305	DQ045305 Homo sapi
3	666.4	80.2	693	5	EX089912	EX089912 EX089912
C 4	376	45.2	587	1	AA527161	AA527161 nt07c12.s
5	367.6	44.2	558	8	DN401602	DN401602 LIBA004-0
C 6	363	43.7	508	1	AA527065	AA527065 nt06g12.s
C 7	343.6	41.3	627	5	AX914278	AX914278 BX914278
8	308.2	37.1	314	8	DN955825	DN955825 TC124474
C 9	256.4	30.9	402	1	AA505489	AA505489 mh96c03.s
10	229	27.6	526	2	BG211784	BG211784 RST31353
C 11	167.4	20.1	530	2	BF875718	BF875718 QV3-ET010
C 12	148.2	17.8	251	1	AA353061	AA353061 EST61135
C 13	138.4	16.7	272	7	CV307751	CV307751 tj46f07.b
C 14	138.4	16.7	272	7	CV307752	CV307752 tj46f07.g
C 15	136.6	16.4	243	7	CV307662	CV307662 tj46a07.b
C 16	136.6	16.4	243	7	CV307663	CV307663 tj46a07.g
C 17	136	16.4	241	7	CV307731	CV307731 tj46e07.b
C 18	136	16.4	241	7	CV307732	CV307732 tj46e07.g
C 19	135.6	16.3	239	7	CV305235	CV305235 tj46g07.b
C 20	135.6	16.3	239	7	CV305236	CV305236 tj46g07.g
C 21	135.6	16.3	239	7	CV307711	CV307711 tj46d07.b
C 22	135.6	16.3	239	7	CV307712	CV307712 tj46d07.g

23	135.6	16.3	239	7	CV307772	CV307772 tj46g07.b
C 24	135.6	16.3	239	7	CV307773	CV307773 tj46g07.g
25	131	15.8	315	7	CN446831	CN446831 tj46b07.s
C 26	131	15.8	315	7	CV307678	CV307678 tj46b07.b
C 27	116	14.0	263	1	AW512550	AW512550 xx64d09.x
C 28	102.4	12.3	238	3	BQ332892	BQ332892 QV3-ET010
C 29	100.6	12.1	275	5	BQ377877	BQ377877 QV1-UM003
30	92.4	11.1	94	11	DQ045306	DQ045306 Pan trogl
31	80.8	9.7	519	9	AQ248174	AQ248174 HS-2045_B
32	76.4	9.2	511	10	CE708684	CE708684 tigr-gss-
C 33	76.4	9.2	680	9	CE116328	CE116328 tigr-gss-
C 34	64.8	7.8	658	9	B2224666	B2224666 CH230-496
C 35	54	6.5	585	2	B1056269	B1056269 PMO-GN034
36	42.6	5.1	602	6	CA727769	CA727769 wdlic.pk0
37	40.8	4.9	658	6	CA497669	CA497669 WHB3230_G
38	40.4	4.9	226	6	CF250573	CF250573 esaa014_d0
C 39	40.2	4.8	936	6	CB953913	CB953913 AGENCOURT
40	39.6	4.8	790	2	BF537732	BF537732 602054426
41	39.4	4.7	565	10	CNS0235A	AL199783 Tetraodon
42	39.4	4.7	629	6	CA596296	CA596296 wpaic.pk0
43	39.4	4.7	1780	4	CNS060T3	CR728177 Tetraodon
44	39.2	4.7	1145	6	CD506105	CD506105 CDA77-D07
45	39.2	4.7	1379	2	BG396489	BG396489 602459217

#### ALIGNMENTS

RESULT 1  
HS804486  
LOCUS HSM804486 3809 bp mRNA linear HTC 16-APR-2005  
DEFINITION Homo sapiens mRNA; cDNA DKFP667A205 (from clone DKFP667A205).  
ACCESSION AL833175  
VERSION AL833175.1 GI:21733802  
KEYWORDS HTC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 3809)  
AUTHORS Bloeker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B., Amid,C.,  
Osanger,A., Fobo,G., Han,M. and Wiemann,S.  
CONSRMT The German cDNA Consortium  
TITLE Direct Submission  
JOURNAL Submitted (20-JAN-2005) MIPS, Ingolstaedter Landstr.1, D-85764  
Neuherberg, GERMANY  
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by GBF (National Research Centre for Biotechnology Ltd.,  
Braunschweig/Germany) within the cDNA sequencing consortium of the  
German Genome Project.  
This clone (DKFP667A205) is available at the RZPD Deutsches  
Resourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.  
Please contact RZPD for ordering:  
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFP667A205  
Further information about the clone and the sequencing project is  
available at http://mips.gsf.de/projects/cdna/.

FEATURES  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="RZPD:DKFP667A205"  
/db\_xref="taxon:9606"  
/clone="DKFP667A205"  
/tissue\_type="lymph node"  
CD10B; sites NotI + SalI  
/dev\_stage="adult"  
/note="hypothetical protein"  
1..3809  
/gene="DKFP667A205"  
2616..3551  
CDS





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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 20:55:02 ; Search time 827 Seconds  
(without alignments)  
8309.375 Million cell updates/sec

Title: US-10-658-482-1

Perfect score: 831

Sequence: 1 cgtctatctgcagtcggtc.....caaccagagggcatctctcgg 831

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

- 1: /cgn2\_6/prodata/1/pubnpna/US07\_PUBCOMB.seq\*
- 2: /cgn2\_6/prodata/1/pubnpna/US08\_PUBCOMB.seq\*
- 3: /cgn2\_6/prodata/1/pubnpna/US09A\_PUBCOMB.seq\*
- 4: /cgn2\_6/prodata/1/pubnpna/US09B\_PUBCOMB.seq\*
- 5: /cgn2\_6/prodata/1/pubnpna/US10A\_PUBCOMB.seq\*
- 6: /cgn2\_6/prodata/1/pubnpna/US10B\_PUBCOMB.seq\*
- 7: /cgn2\_6/prodata/1/pubnpna/US10C\_PUBCOMB.seq\*
- 8: /cgn2\_6/prodata/1/pubnpna/US10D\_PUBCOMB.seq\*
- 9: /cgn2\_6/prodata/1/pubnpna/US10E\_PUBCOMB.seq\*
- 10: /cgn2\_6/prodata/1/pubnpna/US11\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	796	95.8	860	US-10-370-715B-499	Sequence 499, App
2	785.8	94.6	2139	US-10-108-260A-1740	Sequence 1740, App
3	775.8	93.4	1500	US-10-128-558-15	Sequence 15, Appl
C 4	376	45.2	587	US-10-756-149-1939	Sequence 1939, App
C 5	203.4	24.5	247	US-09-796-692-9142	Sequence 9142, App
C 6	203.4	24.5	247	US-10-040-862-9142	Sequence 9142, App
C 7	203.4	24.5	247	US-10-057-475B-9142	Sequence 9142, App
C 8	203.4	24.5	247	US-10-154-884B-9142	Sequence 9142, App
C 9	203.4	24.5	247	US-10-764-324-9142	Sequence 9142, App
10	79	9.5	294	US-10-574-124A-5607	Sequence 5607, App
11	40.6	4.9	1590	US-10-282-122A-31781	Sequence 31781, A
12	36.8	4.4	693	US-10-123-155-406	Sequence 406, App
13	36.8	4.4	693	US-10-146-731-406	Sequence 406, App
14	36.8	4.4	693	US-10-140-472-406	Sequence 406, App
15	36.8	4.4	693	US-10-141-761-406	Sequence 406, App
16	36.8	4.4	693	US-10-142-885-406	Sequence 406, App
17	36.8	4.4	693	US-10-158-790-406	Sequence 406, App
18	36.8	4.4	693	US-10-137-871-406	Sequence 406, App
19	36.8	4.4	693	US-10-140-923-406	Sequence 406, App
20	36.8	4.4	693	US-10-141-756-406	Sequence 406, App
21	36.8	4.4	693	US-10-141-759-406	Sequence 406, App
22	36.8	4.4	693	US-10-140-805-406	Sequence 406, App
23	36.8	4.4	693	US-10-140-864-406	Sequence 406, App

24	36	4.3	993	3	US-09-154-750A-69	Sequence 69, Appl
25	36	4.3	993	3	US-09-880-107-3943	Sequence 3943, App
26	36	4.3	993	3	US-09-968-007A-453	Sequence 453, App
27	36	4.3	993	8	US-10-802-432-28	Sequence 28, Appl
28	36	4.3	993	8	US-10-723-860-1071	Sequence 1071, App
29	36	4.3	993	9	US-10-843-641A-6923	Sequence 6923, App
C 30	36	4.3	1049	5	US-10-123-155-358	Sequence 358, App
C 31	36	4.3	1049	6	US-10-146-731-358	Sequence 358, App
C 32	36	4.3	1049	6	US-10-140-472-358	Sequence 358, App
C 33	36	4.3	1049	6	US-10-141-761-358	Sequence 358, App
C 34	36	4.3	1049	6	US-10-142-885-358	Sequence 358, App
C 35	36	4.3	1049	6	US-10-158-790-358	Sequence 358, App
C 36	36	4.3	1049	6	US-10-137-871-358	Sequence 358, App
C 37	36	4.3	1049	6	US-10-140-923-358	Sequence 358, App
C 38	36	4.3	1049	6	US-10-141-756-358	Sequence 358, App
C 39	36	4.3	1049	6	US-10-141-759-358	Sequence 358, App
C 40	36	4.3	1049	6	US-10-140-805-358	Sequence 358, App
C 41	36	4.3	1049	6	US-10-140-864-358	Sequence 358, App
42	35.8	4.3	26729	6	US-10-283-247-6	Sequence 6, Appl
43	35.8	4.3	26729	10	US-11-143-787-6	Sequence 6, Appl
44	35.8	4.3	70383	6	US-10-283-247-3	Sequence 3, Appl
45	35.8	4.3	70383	10	US-11-143-787-3	Sequence 3, Appl

#### ALIGNMENTS

#### RESULT 1

US-10-370-715B-499  
; Sequence 499, Application US/10370715B  
; Publication No. US20040258678A1  
; GENERAL INFORMATION:  
; Patin Docket Preview  
; APPLICANT: BODARY, SARAH C.  
; APPLICANT: CLARK, HILLARY  
; APPLICANT: BRISDELL, HUNTE  
; APPLICANT: JACKMAN, JANET  
; APPLICANT: SCHOENFELD, JILL R.  
; APPLICANT: WILLIAMS, P. MICKEY  
; APPLICANT: WOOD, WILLIAM I.  
; APPLICANT: WU, THOMAS D.  
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune  
; TITLE OF INVENTION: Related Diseases  
; FILE REFERENCE: P1948R1-US  
; CURRENT APPLICATION NUMBER: US/10/370,715B  
; CURRENT FILING DATE: 2003-02-21  
; NUMBER OF SEQ ID NOS: 742  
; SEQ ID NO 499  
; LENGTH: 860  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-370-715B-499

Query Match 95.8%; Score 796; DB 8; Length 860;  
Best Local Similarity 100.0%; Pred. No. 6.2e-252;  
Matches 796; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	36	AGAGGCCACATCTGCTTCTCTGTAGGCCCTCTCGGAGAGCATGGCTGGTGTCTCTCC	95
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QY	96	TGATCTGGGCCCCAGGGGCTGAGGAGGCTCCCTCGCTCAGGAATGATGACAGGCACAA	155
Db	61	TGATCTGGGCCCCAGGGGCTGAGGAGGCTCCCTCGCTCAGGAATGATGACAGGCACAA	120
QY	156	TAGAAACAAACGGGGAACATTTCTGAGAGAAAGGTGGCTCTATCTTACATGTCTCACC	215
Db	121	TAGAAACAAACGGGGAACATTTCTGAGAGAAAGGTGGCTCTATCTTACATGTCTCACC	180
QY	216	TCTCTCCACACGGCACAAGTGACCCAGGTCAACTGGGAGCAGGACGAGCTTCTGG	275
Db	181	TCTCTCCACACGGCACAAGTGACCCAGGTCAACTGGGAGCAGGACGAGCTTCTGG	240



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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 21:05:04 ; Search time 385 Seconds  
(without alignments)  
4732.351 Million cell updates/sec

Title: US-10-658-482-1

Perfect score: 831

Sequence: 1 cgtctatctgcagtcgct.....caaccagaggaatctctgg 831

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 14437070

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA\_New.\*

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- 2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US03\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
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- 12: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	35.6	4.3	340000	12	US-11-102-978-3
C 2	34.8	4.2	1285	8	US-10-750-185-54718
C 3	34.8	4.2	1285	8	US-10-750-623-54718
C 4	34.8	4.2	1694	8	US-10-689-742-49
C 5	34.8	4.2	3187	8	US-10-947-249-189
C 6	34.6	4.2	142605	12	US-11-121-086-64
C 7	34.2	4.1	1125000	8	US-10-995-561-13286
C 8	34	4.1	801	6	US-09-925-065A-63566
C 9	34	4.1	801	6	US-09-925-065A-63567
C 10	34	4.1	3807	12	US-11-136-527-2151
C 11	33.8	4.1	1558	9	US-11-245-147-192
C 12	33.6	4.0	37507	8	US-10-522-037-2
C 13	33.4	4.0	44617	7	US-10-330-773-928
C 14	33.2	4.0	201	8	US-10-995-561-9475
C 15	33.2	4.0	201	8	US-10-995-561-9486
C 16	33.2	4.0	201	8	US-10-995-561-9497
C 17	33.2	4.0	201	8	US-10-995-561-9513
C 18	33.2	4.0	201	8	US-10-995-561-9527
C 19	33.2	4.0	201	8	US-10-995-561-51204
C 20	33.2	4.0	2333	8	US-10-995-561-343

21	33.2	4.0	2553	8	US-10-995-561-344	Sequence 344, App
22	33.2	4.0	2748	8	US-10-995-561-348	Sequence 348, App
23	33.2	4.0	3287	8	US-10-995-561-346	Sequence 346, App
24	33.2	4.0	3759	8	US-10-995-561-347	Sequence 347, App
25	33.2	4.0	30192	8	US-10-995-561-13306	Sequence 13306, A
26	33	4.0	595	12	US-11-000-688-1158	Sequence 1158, App
27	33	4.0	1620	12	US-11-198-819-11	Sequence 11, Appl
C 28	33	4.0	2310	6	US-09-925-065A-73307	Sequence 73307, A
C 29	32.8	3.9	549	6	US-09-925-065A-805796	Sequence 805796,
C 30	32.8	3.9	549	6	US-09-925-065A-805797	Sequence 805797,
C 31	32.8	3.9	549	6	US-09-925-065A-858007	Sequence 858007,
C 32	32.8	3.9	1101	12	US-11-000-463-221	Sequence 221, App
C 33	32.8	3.9	1788	8	US-10-750-185-61919	Sequence 61919, A
C 34	32.8	3.9	1788	8	US-10-750-623-61919	Sequence 61919, A
C 35	32.8	3.9	2663	12	US-11-000-463-693	Sequence 693, App
C 36	32.8	3.9	34680	12	US-11-124-368A-2903	Sequence 2903, App
C 37	32.4	3.9	555	6	US-09-925-065A-265902	Sequence 265902,
C 38	32.4	3.9	1492	8	US-10-750-185-26396	Sequence 26396, A
C 39	32.4	3.9	1492	8	US-10-750-623-26396	Sequence 26396, A
C 40	32.4	3.9	1755	8	US-10-750-185-43052	Sequence 43052, A
C 41	32.4	3.9	1755	8	US-10-750-623-43052	Sequence 43052, A
C 42	32.4	3.9	153142	12	US-11-121-086-37	Sequence 27, Appl
C 43	32.2	3.9	201	12	US-11-124-368A-2951	Sequence 2951, App
C 44	32.2	3.9	425	6	US-09-925-065A-282462	Sequence 282462,
C 45	32.2	3.9	603	6	US-09-925-065A-42254	Sequence 42254, A

ALIGNMENTS

RESULT 1

US-11-102-978-3/c  
; Sequence 3, Application US/11102978  
; Publication No. US20050250142A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Technology Transfer Office  
; TITLE OF INVENTION: Diagnosis and Treatment of Herpes Simplex Virus Disease  
; FILE REFERENCE: 0274-5537.1US  
; CURRENT APPLICATION NUMBER: US/11/102, 978  
; CURRENT FILING DATE: 2005-04-11  
; PRIOR APPLICATION NUMBER: PCT/US2003/033152  
; PRIOR FILING DATE: 2003-10-18  
; PRIOR APPLICATION NUMBER: 60/419, 576  
; PRIOR FILING DATE: 2002-10-18  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 340000  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: (56948)..(57115)  
; OTHER INFORMATION: C21orf34 exon  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (80006)..(81089)  
; OTHER INFORMATION: Gene VDACC2P; voltage-dependent anion channel isoform 2 pseudogene  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: (167308)..(167438)  
; OTHER INFORMATION: C21orf34 exon  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: (216732)..(216933)  
; OTHER INFORMATION: C21orf34 exon  
US-11-102-978-3

Query Match 4.3%; Score 35.6; DB 12; Length 340000;  
Best Local Similarity 54.6%; Pred. No. 22;  
Matches 71; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 615 GGAAGAAATCAGCTGGACAGGAGGAATGGAGCCCAAGTGTCTCCCTCACCCCGAGGAGCT 674  
Db 81286 GAAACATTCAGGCTGCAAGTGGAAATGTGCTCCACTTTGTCTCCAGTCGAGGAGCT 81227  
QY 675 GTGTCCAGGACAGCTGCACTGTCTGGGCTCTGTGGAGAGCAGCGGGGAGAGACTGTG 734  
Db 81226 GTACCCCAACAGCAGGCAAAACCCAGTGGCTGCTGTGAGCAGCAGCAGTGGGAGCACCC 81167  
QY 735 CCGAGCTGCA 744  
Db 81166 CCCATCTGGA 81157

## RESULT 2

US-10-750-185-54718  
; Sequence 54718, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: FANTIN, Dennis  
; APPLICANT: BATES, Stephen  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 54718  
; LENGTH: 1285  
; TYPE: DNA  
; ORGANISM: Bovine 19866880902223  
US-10-750-185-54718

Query Match 4.2%; Score 34.8; DB 8; Length 1285;

Best Local Similarity 53.7%; Pred. No. 7.9;  
Matches 72; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 47 CTGCTCTCTAGGCGCTCTGGCAGAGCATGCGCTGTGTCTCTCTCTGATCTGGCC 106  
Db 49 CTGTGACGTGAGCACTGTAGCAGAACCAAGAGCGCAAGCCAGGTGCTCAGGCA 108  
QY 107 CAGGGGCTGAGGCGCTCCCTCGCTCAGGAATGATGACAGGCACAATAGAAACAACG 166  
Db 109 CAGGACAGAGCGCTCCGCTGCTCCCTCATCATTTTGTGATGGCCCACTAAGACTACCT 168  
QY 167 GGGAACTTTCTGC 180  
Db 169 CAGACCAATAAAGC 182

## RESULT 3

US-10-750-623-54718  
; Sequence 54718, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482

; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 54718  
; LENGTH: 1285  
; TYPE: DNA  
; ORGANISM: Bovine 19866880902223  
US-10-750-623-54718

Query Match 4.2%; Score 34.8; DB 8; Length 1285;

Best Local Similarity 53.7%; Pred. No. 7.9;  
Matches 72; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 47 CTGCTCTCTAGGCGCTCTGGCAGAGCATGCGCTGTGTCTCTCTCTGATCTGGCC 106  
Db 49 CTGTGACGTGAGCACTGTAGCAGAACCAAGAGCGCAAGCCAGGTGCTCAGGCA 108  
QY 107 CAGGGGCTGAGGCGCTCCCTCGCTCAGGAATGATGACAGGCACAATAGAAACAACG 166  
Db 109 CAGGACAGAGCGCTCCGCTGCTCCCTCATCATTTTGTGATGGCCCACTAAGACTACCT 168  
QY 167 GGGAACTTTCTGC 180  
Db 169 CAGACCAATAAAGC 182

## RESULT 4

US-10-689-742-49  
; Sequence 49, Application US/10689742  
; Publication No. US20050250180A1  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: McCoy, John M  
; APPLICANT: LaVallie, Edward R  
; APPLICANT: Racie, Lisa A  
; APPLICANT: Evans, Cheryl  
; APPLICANT: Merberg, David  
; APPLICANT: Treacy, Maurice  
; APPLICANT: Spaulding, Vikki  
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
; FILE REFERENCE: 00766.000091.10  
; CURRENT APPLICATION NUMBER: US/10/689,742  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 09/746,783  
; PRIOR FILING DATE: 2000-12-21  
; NUMBER OF SEQ ID NOS: 231  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 49  
; LENGTH: 1694  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-689-742-49

Query Match 4.2%; Score 34.8; DB 8; Length 1694;

Best Local Similarity 60.6%; Pred. No. 8.5;  
Matches 57; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 123 CTCCCTCGCTCAGGAATGATGACAGGCACAATAGAAACAACGGGAACATTTCTGCAG 182  
Db 791 CACCCCTTTCTCATTTGACAATGACGGGAACATTGAGAACACACAGAGAAGCTGCAGTACAG 850  
QY 183 AGAAAGTGTCTCTATCATCTTACATGTCACCT 216  
Db 851 TGGTGAGAGGCTCTATAGTTTACAGTGACGT 884

## RESULT 5

US-10-947-249-189  
; Sequence 189, Application US/10947249  
; Publication No. US20050287541A1  
; GENERAL INFORMATION:  
; APPLICANT: Akira NAKAGAWARA  
; APPLICANT: Miki OHIRA

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 4, 2006, 05:57:23 ; Search time 230 Seconds  
(without alignments)  
748.474 Million cell updates/sec

Title: US-10-658-482-2

Perfect score: 1286

Sequence: 1 MWKCLLIWAQGLRQAPLAS.....YFNVLSYSLGNCSPFTETG 244

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues.

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1286	100.0	311	2 Q5JPD8_HUMAN	Q5jpd8 homo sapien
2	1281	99.6	244	2 Q8N877_HUMAN	Q8n877 homo sapien
3	756	58.8	150	2 Q6MZS2_HUMAN	Q6mzs2 homo sapien
4	140.5	10.9	510	2 Q96NY8_HUMAN	Q96ny8 homo sapien
5	138	10.7	508	2 Q8CED8_MOUSE	Q8ced8 mus musculu
6	137	10.7	483	2 Q8DBP8_MOUSE	Q8dbp8 mus musculu
7	137	10.7	508	2 Q8R007_MOUSE	Q8r007 mus musculu
8	133.5	10.4	510	2 Q96K15_HUMAN	Q96k15 homo sapien
9	131.5	10.2	510	2 Q5B929_BOVIN	Q5b929 bos taurus
10	126	9.8	563	2 Q5FWR8_XENTR	Q5fwr8 xenopus tro
11	125	9.7	336	2 Q46551_XPRIM	Q46551 hyllobates s
12	123.5	9.6	114	2 Q8HYT0_MOGWO	Q8hyt0 mogera wogu
13	123	9.6	105	2 Q8HYT6_RABIT	Q8hyt6 oryctolagus
14	122.5	9.5	467	2 Q8CF62_MOUSE	Q8cf62 mus musculu
15	122.5	9.5	530	1 PVR2_MOUSE	P32507 mus musculu
16	122.5	9.5	530	2 Q80XJ5_MOUSE	Q80xj5 mus musculu
17	122.5	9.5	530	2 Q5FVC5_RAT	Q5fvc5 rattus norv
18	122	9.5	159	2 Q72458_HUMAN	Q72458 homo sapien
19	122	9.5	479	2 Q6IB16_HUMAN	Q6ib16 homo sapien
20	122	9.5	538	1 PVR2_HUMAN	Q92692 homo sapien
21	120	9.3	215	2 Q6T3V1_CTEID	Q6t3v1 ctenopharyn
22	118.5	9.2	336	1 CD226_HUMAN	Q15762 homo sapien
23	118	9.2	1209	2 Q4SF88_TETNG	Q4sf88 tetraodon n
24	117	9.1	483	2 Q4RRK0_TETNG	Q4rrk0 tetraodon n
25	117	9.1	485	2 Q4RRC2_TETNG	Q4rrc2 tetraodon n
26	116.5	9.1	114	2 Q8HYU0_BOVIN	Q8hyu0 bos taurus
27	116.5	9.1	467	2 Q91VT9_MOUSE	Q91vt9 mus musculu
28	115.5	9.0	114	2 Q8HYT2_TURTR	Q8hyt2 tursiops tr
29	115.5	9.0	463	2 Q6GJ72_XENLA	Q6gj72 xenopus lae
30	114.5	8.9	254	2 Q5ZKJ6_CHICK	Q5zkj6 gallus gall
31	113.5	8.8	1165	2 Q5USA3_XENLA	Q5usa3 xenopus lae

32	113	8.8	267	2 Q8NC05_HUMAN	Q8nc05 homo sapien
33	113	8.8	306	2 Q4SMD1_TETNG	Q4smd1 tetraodon n
34	113	8.8	345	2 Q5ZKE7_CHICK	Q5zke7 gallus gall
35	113	8.8	412	2 Q8HY14_RABIT	Q8hy14 oryctolagus
36	113	8.8	515	1 PVR1_MOUSE	Q9jkkf6 mus musculu
37	113	8.8	515	2 Q6P9M9_MOUSE	Q6p9m9 mus musculu
38	113	8.8	588	2 Q6IR66_XENLA	Q6ir66 xenopus lae
39	112.5	8.7	114	2 Q8HYT4_CANFA	Q8hyt4 canis famli
40	112.5	8.7	449	2 Q9UEI6_HUMAN	Q9uei6 homo sapien
41	112	8.7	336	1 CD226_MACMU	O18906 macaca mula
42	111.5	8.7	220	2 Q8K4E3_MOUSE	Q8k4e3 mus musculu
43	111.5	8.7	333	1 CD226_MOUSE	Q8k4f0 mus musculu
44	111.5	8.7	333	2 Q5DW69_MOUSE	Q5dw69 mus musculu
45	111	8.6	190	2 Q4S8A2_TETNG	Q4s8a2 tetraodon n

## ALIGNMENTS

### RESULT 1

Q5JPD8\_HUMAN PRELIMINARY; PRT; 311 AA.  
AC Q5JPD8;  
DT 10-MAY-2005 (TREMELrel. 30, Created)  
DT 10-MAY-2005 (TREMELrel. 30, Last sequence update)  
DT 10-MAY-2005 (TREMELrel. 30, Last annotation update)  
DE Hypothetical protein DKFZp667A205.  
GN Name=DKFZp667A205;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lymph node;  
RG The German cDNA Consortium;  
RA Bloecker H., Boecker M., Brandt P., Mewes H.W., Weil B., Amid C.,  
RA Osanger A., Fobo G., Han M., Wiemann S.;  
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL833175; CAI46183.1; -; mRNA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR SMART; SM00409; IG; 1.  
DR PROSITE; P850835; IG LIKE; 1.  
KW Hypothetical protein; Immunoglobulin domain.  
SQ SEQUENCE 311 AA; 33926 MW; AA9E9E3944DCB3EB CRC64;

Query Match 100.0%; Score 1286; DB 2; Length 311;  
Best Local Similarity 100.0%; Pred. No. 3e-103;  
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MWCLLLIWAQGLRQAPLASGMWMTGTTFTGNISAEKGGSIILQCHLSSTTAQVTVNWE	60
Db	68	MWCLLLIWAQGLRQAPLASGMWMTGTTFTGNISAEKGGSIILQCHLSSTTAQVTVNWE	127
QY	61	QDQLLAIACNADLGHWSFSDRVAPGPGGLGLTLQSLTVNDTGEYFCIYHYTPDGTG	120
Db	128	QDQLLAIACNADLGHWSFSDRVAPGPGGLGLTLQSLTVNDTGEYFCIYHYTPDGTG	187
QY	121	RIFLEVLSSVAEHGARGFOIPLLGMAATLVVICTAVIVVVALTRKKKALRHSVEGDLR	180
Db	188	RIFLEVLSSVAEHGARGFOIPLLGMAATLVVICTAVIVVVALTRKKKALRHSVEGDLR	247
QY	181	RSAGQEEWSPSPGSCVQAEAPAGLCGEQGEDCAELHDYFNVLSYSLGNCSPF	240
Db	248	RSAGQEEWSPSPGSCVQAEAPAGLCGEQGEDCAELHDYFNVLSYSLGNCSPF	307
QY	241	TETG 244	
Db	308	TETG 311	

```
RESULT 2
Q8N877_HUMAN
ID Q8N877_HUMAN PRELIMINARY; PRT; 244 AA.
AC Q8N877;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ39873.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoaka S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hotta T.,
RA Kusano J., Kanehori K., Takahashi F., Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Inose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshioka Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzawa Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami S., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs."
RL Nat. Genet. 36:40-45(2004).
DR EMBL; AK097192; BAC04973.1; -; mRNA.
DR Ensembl; ENSG00000181847; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 244 AA; 26289 MW; F98CDF73F604B858 CRC64;

Query Match 99.6%; Score 1281; DB 2; Length 244;
Best Local Similarity 99.6%; Pred. No. 6.1e-103;
Matches 243; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRWCLLIWAQGLRQAPLQAGMTGTTTGNISAEKGGSIILQCHLSSTTAQVTQNW 60
DB 1 MRWCLLIWAQGLRQAPLQAGMTGTTTGNISAEKGGSIILQCHLSSTTAQVTQNW 60
QY 61 QQQDQLLAICNADLGWHTSPFKDRAVPGGLGLTLQSLTVNDTGEYFCIYHTYPDGNYTG 120
DB 61 QQQDQLLAICNADLGWHTSPFKDRAVPGGLGLTLQSLTVNDTGEYFCIYHTYPDGNYTG 120
QY 121 RIFLEVLSSVAEHGAFQIPLLGAMAATLVICTAVIVVVALTRKKKALRIHVSVDLRL 180
DB 121 RIFLEVLSSVAEHGAFQIPLLGAMAATLVICTAVIVVVALTRKKKALRIHVSVDLRL 180

RESULT 3
Q6MZS2_HUMAN
ID Q6MZS2_HUMAN PRELIMINARY; PRT; 150 AA.
AC Q6MZS2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp667N0215 (Fragment).
GN Name=DKFZp667N0215;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph node;
RA Ottenwaelder B., Obermaier B., Deutschenbaur S., Mewes H.W., Weil B.,
RA Anid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640915; CAE45956.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 150 AA; 16123 MW; E4756449EBC92482 CRC64;

Query Match 58.8%; Score 756; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.4e-57;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 GMMTGTIETGNISAEKGGSIILQCHLSSTTAQVTQNWNEQDQLLAICNADLGWHTSPS 80
DB 1 GMMTGTIETGNISAEKGGSIILQCHLSSTTAQVTQNWNEQDQLLAICNADLGWHTSPS 60
QY 81 FKDRVAPGPGGLGLTLQSLTVNDTGEYFCIYHTYPDGTYTGRIFLEVLSSVAEHGAFQI 140
DB 61 FKDRVAPGPGGLGLTLQSLTVNDTGEYFCIYHTYPDGTYTGRIFLEVLSSVAEHGAFQI 120
QY 141 PLLGAMAATLVICTAVIVVVALTRK 166
DB 121 PLLGAMAATLVICTAVIVVVALTRK 146

RESULT 4
Q96NY8_HUMAN
ID Q96NY8_HUMAN PRELIMINARY; PRT; 510 AA.
AC Q96NY8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Nectin 4 (PVRL4 protein) (Poliovirus receptor-related 4).
GN Name=PVRL4; ORFNames=RP11-544M22.7-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21560925; PubMed=11544254; DOI=10.1074/jbc.M103810200;

QY 1 MRWCLLIWAQGLRQAPLQAGMTGTTTGNISAEKGGSIILQCHLSSTTAQVTQNW 60
DB 1 MRWCLLIWAQGLRQAPLQAGMTGTTTGNISAEKGGSIILQCHLSSTTAQVTQNW 60
QY 61 QQQDQLLAICNADLGWHTSPFKDRAVPGGLGLTLQSLTVNDTGEYFCIYHTYPDGNYTG 120
DB 61 QQQDQLLAICNADLGWHTSPFKDRAVPGGLGLTLQSLTVNDTGEYFCIYHTYPDGNYTG 120
QY 121 RIFLEVLSSVAEHGAFQIPLLGAMAATLVICTAVIVVVALTRKKKALRIHVSVDLRL 180
DB 121 RIFLEVLSSVAEHGAFQIPLLGAMAATLVICTAVIVVVALTRKKKALRIHVSVDLRL 180
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 4, 2006, 05:56:48 ; Search time 188 Seconds  
(without alignments)

570.258 Million cell updates/sec

Title: US-10-658-482-2

Perfect score: 1286

Sequence: 1 MRWCLLIWAQGLRQAPLAS.....YFNVLVSLGNCSPFFETG 244

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Search: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_21.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1286	100.0	244	8	Adm32156 PRO52254
2	1286	100.0	244	8	Adl91492 Human imm
3	1286	100.0	257	7	Adf76825 Novel hum
4	1286	100.0	311	6	Ada21139 Human sec
5	1281	99.6	244	7	Adm05498 Human pro
6	1254.5	97.6	249	7	Adm07984 Novel pro
7	1254.5	97.6	249	9	Adm040354 Novel hum
8	1178.5	91.6	240	7	Adm09032 Novel pro
9	707.5	55.0	241	8	Adm32158 Mouse PRO
10	492.5	38.3	98	4	Agg81431 Human AFP
11	256	19.9	50	5	Abp10156 Human ORF
12	146.5	11.4	498	5	AAE23305 Human nec
13	140.5	10.9	485	8	Adk83283 Human 191
14	140.5	10.9	485	8	Adk83298 Human 191
15	140.5	10.9	485	8	Adk83184 Human 191
16	140.5	10.9	485	8	Adk83202 Human 191
17	140.5	10.9	485	8	Adk83285 Human 191
18	140.5	10.9	497	5	AAE23303 Human nec
19	140.5	10.9	510	4	AAU00471 Human TAN
20	140.5	10.9	510	5	ABJ05562 Breast ca
21	140.5	10.9	510	6	ABR48229 Human bla
22	140.5	10.9	510	6	ABU56613 Lung canc
23	140.5	10.9	510	6	ABP97212 Tumour-as
24	140.5	10.9	510	7	ADB80512 Ovarian c

25	140.5	10.9	510	7	ADM42033	Adm42033 Human TAN
26	140.5	10.9	510	7	ADN38748	Adn38748 Cancer/an
27	140.5	10.9	510	8	ADK83210	Adk83210 Human 191
28	140.5	10.9	510	8	ADK83290	Adk83290 Human 191
29	140.5	10.9	510	8	ADK83209	Adk83209 Human 191
30	140.5	10.9	510	8	ADK83284	Adk83284 Human 191
31	140.5	10.9	510	8	ADK83172	Adk83172 Human 191
32	140.5	10.9	510	8	ADK83174	Adk83174 Human 191
33	140.5	10.9	510	8	ADK83176	Adk83176 Human 191
34	140.5	10.9	510	8	ADK83194	Adk83194 Human 191
35	140.5	10.9	510	8	ADK83180	Adk83180 Human 191
36	140.5	10.9	510	8	ADK83291	Adk83291 Human 191
37	140.5	10.9	510	8	ADK83200	Adk83200 Human 191
38	140.5	10.9	510	8	ADK83199	Adk83199 Human 191
39	140.5	10.9	510	8	ADK83205	Adk83205 Human 191
40	140.5	10.9	510	8	ADK83251	Adk83251 Human 191
41	140.5	10.9	510	8	ADK83289	Adk83289 Human 191
42	140.5	10.9	510	8	ADK83296	Adk83296 Human 191
43	140.5	10.9	510	8	ADK83186	Adk83186 Human 191
44	140.5	10.9	510	8	ADK83178	Adk83178 Human 191
45	140.5	10.9	510	8	ADK83211	Adk83211 Human 191

#### ALIGNMENTS

#### RESULT 1

ADM32156

ID ADM32156 standard; protein; 244 AA.

XX AC ADM32156;

XX AC ADM32156;

DT 17-JUN-2004 (first entry)

DE PRO52254 amino acid sequence, seq id 2.

KW Immunosuppressive; dermatological; hepatotropic; nephrotropic;

KW antidiabetic; antiaslathmic; antipsoriatic; antiallergic; antianemic;

KW antiarteriosclerotic; antiarthritic; neuroprotective; respiratory;

KW antiinflammatory; gene therapy; rheumatoid arthritis; asthma.

XX OS Unidentified.

XX PN WO2004024068-A2.

XX PD 25-MAR-2004.

XX PF '09-SEP-2003; 2003WO-US028202.

XX PR 11-SEP-2002; 2002US-0410062P.

XX PA (GETH ) GENENTECH INC.

XX PI Baldwin DT, Bodary SC, Chan AC, Clark H, Jackman JK, Wood WI;

XX DR WPI; 2004-269871/25.

XX DR N-PSDB; ADM32155.

XX PT New PRO52254 nucleic acid or polypeptide, useful for preparing a

XX PT composition for diagnosing or treating in a mammal an immune related

XX PS disorder e.g. systemic lupus erythematosus.

XX PS Claim 3; SEQ ID NO 2; 100pp; English.

XX CC The invention relates to an isolated PRO52254 nucleic acid. Further

XX CC disclosed is a vector comprising the nucleic acid. The PRO52254 nucleic

XX CC acid or polypeptide is useful for preparing a composition for diagnosing

XX CC or treating an immune related disorder, e.g., systemic lupus

XX CC erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic

XX CC arthritis, spondyloarthropathy, systemic sclerosis, idiopathic

XX CC inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,

XX CC sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia,

XX CC thyroiditis, diabetes mellitus, immune-mediated renal disease, a

CC demyelinating disease of the central or peripheral nervous system,  
 CC idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, chronic  
 CC inflammatory demyelinating polyneuropathy, hepatobiliary disease,  
 CC infectious or autoimmune chronic active hepatitis, primary biliary  
 CC cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory  
 CC bowel disease, gluten-sensitive enteropathy, Whipple's disease,  
 CC autoimmune or immune-mediated skin disease, bullous skin disease,  
 CC erythema multiforme, contact dermatitis, psoriasis, allergic disease,  
 CC asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity,  
 CC urticaria, immunologic disease of the lung, eosinophilic pneumonias,  
 CC idiopathic pulmonary fibrosis, hypersensitivity pneumonitis,  
 CC transplantation associated disease, graft rejection or graft-versus-host-  
 CC disease. The current sequence represents the PRO52245 amino acid  
 CC sequence.  
 XX  
 SQ Sequence 244 AA;

Query Match 100.0%; Score 1286; DB 8; Length 244;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-112;  
 Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRWCLLLIWAQGLRQAPLASGMWTGTTTGNISAEKGGSIILQCHLSSTTAQVTQVNW 60  
 DB 1 MRWCLLLIWAQGLRQAPLASGMWTGTTTGNISAEKGGSIILQCHLSSTTAQVTQVNW 60  
 QY 61 QDQLLAINADIGWHISPSFKDRVAPGGLGLTQSLTVNDTGEYFCIYHTYDGTG 120  
 DB 61 QDQLLAINADIGWHISPSFKDRVAPGGLGLTQSLTVNDTGEYFCIYHTYDGTG 120  
 QY 121 RIFLEVLSSVAEHGAFQIPLLCMAATLVICTAVIVVVALTRKKALRIHSVEGDLR 180  
 DB 121 RIFLEVLSSVAEHGAFQIPLLCMAATLVICTAVIVVVALTRKKALRIHSVEGDLR 180  
 QY 181 RKSAGQEWSPSPSPGSCVQAEAPAGLCGQGEDCAELHDYFNVLVSRLGNCSPF 240  
 DB 181 RKSAGQEWSPSPSPGSCVQAEAPAGLCGQGEDCAELHDYFNVLVSRLGNCSPF 240  
 QY 241 TETG 244  
 DB 241 TETG 244

## RESULT 2

ADL91492  
 ID ADL91492 standard; protein; 244 AA.

-XX AC ADL91492;

XX 17-JUN-2004 (first entry)

XX Human immune-related polypeptide PRO52254, SEQ ID NO:7.

XX Human; PRO; activated T cell; immune-related; drug screening; detection;  
 KW stimulation; immune response; stimulation; diagnosis; immune disorder;  
 KW systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis;  
 KW juvenile chronic arthritis; spondyloarthritis; systemic sclerosis;  
 KW idiopathic inflammatory myopathy; Sjogren's syndrome;  
 KW systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia;  
 KW autoimmune thrombocytopenia; thyroiditis; diabetes mellitus;  
 KW immune-mediated renal disease; demyelinating disease;  
 KW idiopathic demyelinating polyneuropathy; Guillain-Barre syndrome;  
 KW chronic inflammatory demyelinating polyneuropathy; hepatobiliary disease;  
 KW chronic active hepatitis; primary biliary cirrhosis;  
 KW granulomatous hepatitis; sclerosing cholangitis;  
 KW inflammatory bowel disease; gluten-sensitive enteropathy;  
 KW Whipple's disease; autoimmune skin disease; immune-mediated skin disease;  
 KW bullous skin disease; erythema multiforme; contact dermatitis; psoriasis;  
 KW allergic disease; asthma; allergic rhinitis; atopic dermatitis;  
 KW food hypersensitivity; urticaria; eosinophilic pneumonitis;  
 KW idiopathic pulmonary fibrosis; hypersensitivity pneumonitis;  
 KW transplantation associated disease; graft rejection;  
 KW graft-versus-host-disease; immunosuppressive; dermatological;  
 KW hepatotropic; nephrotropic; antidiabetic; antiasthmatic; antipsoriatic;

KW anti-allergic; antianaemic; antiarteriosclerotic; antiarthritic;  
 KW neuroprotective; respiratory; antiinflammatory; gene therapy.  
 OS Homo sapiens.

XX WO2004024072-A2.

XX 25-MAR-2004.

XX 10-SEP-2003; 2003WO-US028317.

XX 11-SEP-2002; 2002US-0410340P.

XX (GETH ) GENENTECH INC.

XX Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;

PI Williams PM, Wood WI, Wu TD;

XX WPI; 2004-329384/30.

DR N-PSDB; ADL91491.

XX New PRO nucleic acid, useful for preparing a composition for diagnosing  
 PT or treating an immune related disorder, e.g., systemic lupus  
 PT erythematosus in a mammal.

PS Claim 10; SEQ ID NO 7; 199pp; English.

XX The invention relates to isolated human immune-related polypeptides  
 CC (designated PRO) and nucleic acids (ADL91486-ADL91587). The PRO  
 CC polypeptides are overexpressed in CD4+ T cells activated by anti-CD3/ICAM  
 CC -1 or anti-CD3/anti-CD28 antibodies compared with resting T cells and are  
 CC useful as diagnostic markers and therapeutic targets for immune  
 CC disorders. The invention also relates to sequences of at least 80% identical  
 CC to the PRO nucleic acid and polypeptide sequences of the invention; a  
 CC recombinant vectors and host cells comprising a PRO nucleic acid; a  
 CC method for the recombinant production of a PRO polypeptide; antibodies  
 CC against a PRO polypeptide; fusion proteins comprising a PRO polypeptide;  
 CC methods of screening for compounds which modulate PRO polypeptide  
 CC activity or expression; a method for detecting a PRO polypeptide; a  
 CC method of detecting an immune response in a mammal; a method for  
 CC stimulating an immune response in a mammal; and methods for diagnosing  
 CC and treating immune-related disorders. PRO polypeptides and nucleic acids  
 CC are useful in the diagnosis and treatment of immune-related disorders  
 CC such as systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthritis, systemic  
 CC sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome, autoimmune  
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal  
 CC disease, a demyelinating disease of the central or peripheral nervous  
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,  
 CC chronic inflammatory demyelinating polyneuropathy, hepatobiliary disease,  
 CC infectious or autoimmune chronic active hepatitis, primary biliary  
 CC cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory  
 CC bowel disease, gluten-sensitive enteropathy, Whipple's disease,  
 CC autoimmune or immune-mediated skin disease, bullous skin disease,  
 CC erythema multiforme, contact dermatitis, psoriasis, allergic disease,  
 CC asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity,  
 CC urticaria, immunologic disease of the lung, eosinophilic pneumonias,  
 CC idiopathic pulmonary fibrosis, hypersensitivity pneumonitis,  
 CC transplantation associated disease, graft rejection or graft-versus-host-  
 CC disease. The present sequence represents a human immune-related PRO  
 CC polypeptide of the invention.

XX Sequence 244 AA;

Query Match 100.0%; Score 1286; DB 8; Length 244;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-112;  
 Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRWCLLLIWAQGLRQAPLASGMWTGTTTGNISAEKGGSIILQCHLSSTTAQVTQVNW 60  
 DB 1 MRWCLLLIWAQGLRQAPLASGMWTGTTTGNISAEKGGSIILQCHLSSTTAQVTQVNW 60



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 4, 2006, 06:05:04 ; Search time 166 Seconds  
(without alignments)  
614.159 Million cell updates/sec

Title: US-10-658-482-2  
Perfect score: 1286  
Sequence: 1 MRWCLLLIWAQGLRQAPLAS.....YFNVLSYSLGNCSPFFTTG 244

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

\*Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pcp.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pcp.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pcp.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1286	100.0	257	5	US-10-370-715B-500
2	1281	99.6	244	4	US-10-108-260A-4183
3	1254.5	97.6	249	5	US-10-128-558-139
4	146.5	11.4	498	3	US-09-972-268-39
5	140.5	10.9	485	4	US-10-422-571-15
6	140.5	10.9	485	4	US-10-422-571-33
7	140.5	10.9	485	4	US-10-422-571-114
8	140.5	10.9	485	4	US-10-422-571-116
9	140.5	10.9	485	4	US-10-422-571-129
10	140.5	10.9	497	3	US-09-972-268-37
11	140.5	10.9	510	3	US-09-766-511B-33
12	140.5	10.9	510	4	US-10-241-220-94
13	140.5	10.9	510	4	US-10-295-027-66
14	140.5	10.9	510	4	US-10-173-999-76
15	140.5	10.9	510	4	US-10-058-270A-54
16	140.5	10.9	510	4	US-10-188-832-179
17	140.5	10.9	510	4	US-10-422-571-3
18	140.5	10.9	510	4	US-10-422-571-7
19	140.5	10.9	510	4	US-10-422-571-5
20	140.5	10.9	510	4	US-10-422-571-9
21	140.5	10.9	510	4	US-10-422-571-11
22	140.5	10.9	510	4	US-10-422-571-17
23	140.5	10.9	510	4	US-10-422-571-25
24	140.5	10.9	510	4	US-10-422-571-30
25	140.5	10.9	510	4	US-10-422-571-31
26	140.5	10.9	510	4	US-10-422-571-36
27	140.5	10.9	510	4	US-10-422-571-40

28	140.5	10.9	510	4	US-10-422-571-41	Sequence 41, Appl
29	140.5	10.9	510	4	US-10-422-571-42	Sequence 42, Appl
30	140.5	10.9	510	4	US-10-422-571-82	Sequence 82, Appl
31	140.5	10.9	510	4	US-10-422-571-115	Sequence 115, Appl
32	140.5	10.9	510	4	US-10-422-571-120	Sequence 120, Appl
33	140.5	10.9	510	4	US-10-422-571-121	Sequence 121, Appl
34	140.5	10.9	510	4	US-10-422-571-122	Sequence 122, Appl
35	140.5	10.9	510	4	US-10-422-571-127	Sequence 127, Appl
36	140.5	10.9	510	5	US-10-872-972-94	Sequence 94, Appl
37	140.5	10.9	510	5	US-10-872-991-94	Sequence 94, Appl
38	140.5	10.9	511	4	US-10-422-571-27	Sequence 27, Appl
39	140.5	10.9	511	4	US-10-422-571-37	Sequence 37, Appl
40	138.5	10.8	510	3	US-09-972-268-24	Sequence 24, Appl
41	138.5	10.8	510	3	US-09-829-472A-6	Sequence 6, Appl
42	138.5	10.8	510	4	US-10-161-572-54	Sequence 54, Appl
43	138.5	10.8	510	4	US-10-422-571-23	Sequence 23, Appl
44	138.5	10.8	510	4	US-10-422-571-35	Sequence 35, Appl
45	137.5	10.7	511	3	US-09-972-268-34	Sequence 34, Appl

## ALIGNMENTS

## RESULT 1

US-10-370-715B-500

; Sequence 500, Application US/10370715B

; Publication No. US20040258678A1

; GENERAL INFORMATION:

; Patin Docket Preview

; APPLICANT: BODARY, SARAH C.

; APPLICANT: CLARK, HILLARY

; APPLICANT: BRISDELL, HUNTE

; APPLICANT: JACKMAN, JANET

; APPLICANT: SCHOENFELD, JILL R.

; APPLICANT: WILLIAMS, P. MICKEY

; APPLICANT: WOOD, WILLIAM I.

; APPLICANT: WU, THOMAS D.

; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune

; TITLE OF INVENTION: Related Diseases

; FILE REFERENCE: P1948R1-US

; CURRENT APPLICATION NUMBER: US/10/370,715B

; CURRENT FILING DATE: 2003-02-21

; NUMBER OF SEQ ID NOS: 742

; SEQ ID NO 500

; LENGTH: 257

; TYPE: PRT

; ORGANISM: Homo sapien

; US-10-370-715B-500

Query Match

Best Local Similarity 100.0%; Score 1286; DB 5; Length 257;

Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRWCLLLIWAQGLRQAPLASGMMTGTITTTGNSAEKGGSILOCHLSSTTAQVTVNWE	60
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Qy	61	QDOLLATCNADLGHWSFSDRVAPGPGGLTLOSLTVNDTGYFCIYHTYPDGTG	120
Db	74	QDQLLALCNADLGHWSFSDRVAPGPGGLTLOSLTVNDTGYFCIYHTYPDGTG	133
Qy	121	RIFLEVLSSVAEARGAFQIFLLGMAATLVICTAVIVVVALTRKKALRHSVEGDLR	180
Db	134	RIFLEVLSSVAEARGAFQIFLLGMAATLVICTAVIVVVALTRKKALRHSVEGDLR	193
Qy	181	RKSAGQEWSPSPGSCVQAEAPAGLCEGORGECABELHDFNVLSYSLGNCSPFF	240
Db	194	RKSAGQEWSPSPGSCVQAEAPAGLCEGORGECABELHDFNVLSYSLGNCSPFF	253
Qy	241	TETG 244	
Db	254	TETG 257	

## RESULT 2

US-10-108-260A-4183  
; Sequence 4183, Application US/10108260A  
; Publication No. US20040005560A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: NO US20040005560A1el full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/10/108,260A  
; CURRENT FILING DATE: 2002-03-27  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4183  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-108-260A-4183

Query Match 99.6%; Score 1281; DB 4; Length 244;  
Best Local Similarity 99.6%; Pred. No. 4.6e-107;  
Matches 243; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
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DB 1 MRWCLLLIWAQGLRQAPLASGMWTGTIETTGNSIAEKGGSIILQCHLSSTTAQVTQVNW 60  
  
QY 61 QDQLLAIACNADLGHWHISPSFKDRVAPGPGGLGLTLQSLTVNDTGYFCIYHTYPTDGTG 120  
DB 61 QDQLLAIACNADLGHWHISPSFKDRVAPGPGGLGLTLQSLTVNDTGYFCIYHTYPTDGTG 120  
  
QY 121 RIFLEVLSSVAEHGARGFOIPLLGMAATLVICTAVIVVVALTRKKKALRIHS 180  
DB 121 RIFLEVLSSVAEHGARGFOIPLLGMAATLVICTAVIVVVALTRKKKALRIHS 180  
  
QY 181 RKSAGQEWSPSPGSCVQAEAPAGLCGEQGEDCAELHDYFNVLNLSYRSL 240  
DB 181 RKSAGQEWSPSPGSCVQAEAPAGLCGEQGEDCAELHDYFNVLNLSYRSL 240  
  
QY 241 TETG 244  
DB 241 TETG 244

## RESULT 3

US-10-128-558-139  
; Sequence 139, Application US/10128558  
; Publication No. US20040219521A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: Weng, Gezhi  
; APPLICANT: Boyle, Bryan J  
; APPLICANT: Drmanac, Radoje T  
; TITLE OF INVENTION: Novel Nucleic Acids and  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 812A  
; CURRENT APPLICATION NUMBER: US/10/128,558  
; CURRENT FILING DATE: 2002-04-22  
; PRIOR APPLICATION NUMBER: US 60/339,453  
; PRIOR FILING DATE: 2001-12-11  
; PRIOR APPLICATION NUMBER: US 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: US 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: PCT/US00/35017  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/491,404  
; PRIOR FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: PCT/US01/02623  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: US 09/496,914  
; PRIOR FILING DATE: 2000-02-03

; PRIOR APPLICATION NUMBER: US 09/560,875  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: PCT/US01/03800  
; PRIOR FILING DATE: 2001-02-05  
; PRIOR APPLICATION NUMBER: US 09/515,126  
; PRIOR FILING DATE: 2000-02-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 412  
; SOFTWARE: PCT\_Files Version 6.0  
; SEQ ID NO 139  
; LENGTH: 249  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-128-558-139

Query Match 97.6%; Score 1254.5; DB 5; Length 249;  
Best Local Similarity 96.8%; Pred. No. 1.2e-104;  
Matches 242; Conservative 1; Mismatches 0; Indels 7; Gaps 2;  
  
QY 1 MRWCLLLIWAQGLRQAPLASGMWTGTIETTGNSIAEKGGSIILQCHLSSTTAQVTQVNW 60  
DB 1 MRWCLLLIWAQGLRQAPLASGMWTGTIETTGNSIAEKGGSIILQCHLSSTTAQVTQVNW 60  
  
QY 61 QDQLLAIACNADLGHWHISPSFKDRVAPGPGGLGLTLQSLTVNDTGYFCIYHTYPTDGTG 120  
DB 61 QDQLLAIACNADLGHWHISPSFKDRVAPGPGGLGLTLQSLTVNDTGYFCIYHTYPTDGTG 120  
  
QY 121 RIFLEVLSSVAEHGARGFOIPLLGMAATLVICTAVIVVVALTRKKKALRIHS 174  
DB 121 RIFLEVLSSGIPAGMAEHGARGFOIPLLGMAATLVICTAVIVVVALTR-KKALRIHS 179  
  
QY 175 VEGDLRRSAGQEWSPSPGSCVQAEAPAGLCGEQGEDCAELHDYFNVLNLSYRSL 234  
DB 180 VEGDLRRSAGQEWSPSPGSCVQAEAPAGLCGEQGEDCAELHDYFNVLNLSYRSL 239  
  
QY 235 GNCSEFTTGT 244  
DB 240 GNCSEFTTGT 249

## RESULT 4

US-09-972-268-39  
; Sequence 39, Application US/09972268  
; Publication No. US20030044893A1  
; GENERAL INFORMATION:  
; APPLICANT: Baum, Peter R.  
; APPLICANT: Fanelow, William C.  
; APPLICANT: Lofton, Timothy E.  
; APPLICANT: Sorensen, Eric A.  
; APPLICANT: Youakim, Adel  
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE  
; FILE REFERENCE: 3101-A  
; CURRENT APPLICATION NUMBER: US/09/972,268  
; CURRENT FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: 60/238,557  
; PRIOR FILING DATE: 2000-10-05  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 39  
; LENGTH: 498  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-972-268-39

Query Match 11.4%; Score 146.5; DB 3; Length 498;  
Best Local Similarity 29.0%; Pred. No. 0.0002;  
Matches 51; Conservative 23; Mismatches 63; Indels 39; Gaps 7;  
  
QY 3 WCILLIWAQGLRQAPLASGMWTGTIETTGNSIAEKGGSIILQCHLSSTTAQVTQVNW 61  
DB 27 WLLLL-----LLLSFAGRCPCAGLETSDDVTVVLQDQAKLPCFYRGDSGEQGVQAWAR 81  
  
QY 62 QD-----QLLAICNADLGHWHISPSFKDRV-APGPGGLGL-----TLQSLTVNDTGYFCIY 110

GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Bioacceleration Ltd.  
 OM protein - protein search, using sw model  
 Run on: March 4, 2006, 06:00:28 ; Search time 40 seconds  
 (without alignments)  
 586.922 Million cell updates/sec  
 Title: US-10-658-482-2  
 Perfect score: 1285  
 Sequence: 1 MWKLLLIWAQGLRQAPLAS.....YFNVLSYSLGNCSPFTTGT 244  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
 Total number of hits satisfying chosen parameters: 283416  
 Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000  
 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries  
 Database : PIR 80.\*  
 1: pir1.\*  
 2: pir2.\*  
 3: pir3.\*  
 4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	122.5	9.5	467	1 HLMSP3	poliovirus recepto
2	122.5	9.5	530	2 A53437	poliovirus recepto
3	122	9.5	478	2 I53960	PRR2 alpha - human
4	122	9.5	538	2 I68093	PRR2 delta - human
5	111.5	8.7	518	2 JC4024	poliovirus recepto
6	106.5	8.3	416	2 A54017	colon carcinoma-as
7	104.5	8.1	392	1 RWHPD	poliovirus recepto
8	104.5	8.1	417	1 RWHPA	poliovirus recepto
9	104	8.1	186	2 I61783	sodium channel bet
10	104	8.1	215	2 A57843	sodium channel bet
11	101.5	7.9	304	1 RWCHH7	cell surface glyco
12	100	7.8	108	1 KVM582	ig kappa chain v r
13	100	7.8	114	2 S22559	ig heavy chain v r
14	100	7.8	229	2 A20969	ig kappa chain pre
15	99	7.7	93	2 I47624	ig heavy chain v-v
16	99	7.7	108	1 KVM561	ig kappa chain v r
17	97	7.5	108	1 KVM506	ig kappa chain v r
18	96.5	7.5	572	2 B45529	ig v heavy chain (
19	96	7.5	130	2 S08079	ig kappa chain pre
20	96	7.5	1327	2 T09402	immunoglobulin-lik
21	94.5	7.3	398	2 A93371	ig v-region-like B
22	94	7.3	108	1 KVM509	ig kappa chain v r
23	94	7.3	128	2 S31488	ig kappa chain pre
24	94	7.3	129	2 A30554	ig lambda chain pr
25	94	7.3	381	2 I51174	ig heavy chain - R
26	93.5	7.3	392	2 B44194	poliovirus recepto
27	93.5	7.3	417	2 A44194	poliovirus recepto
28	93	7.2	125	2 S40315	ig kappa chain - h
29	93	7.2	468	1 B46114	glycoprotein gp13

30 93 7.2 468 1 VGBEEH glycoprotein gp13  
 31 92 7.2 103 2 S18731 ig kappa chain v-j  
 32 244 7.2 244 2 A40428 nonspecific cross-  
 33 91.5 7.1 129 1 KIHUWK ig kappa chain pre  
 34 91.5 7.1 569 2 A46462 T cell activation  
 35 90.5 7.0 129 2 S52792 ig kappa chain v r  
 36 89.5 7.0 105 2 S38488 ig heavy chain - h  
 37 89.5 7.0 125 2 S40350 ig kappa chain - h  
 38 89.5 7.0 345 2 JC1239 oploid-binding pro  
 39 89 6.9 210 2 S36297 T-cell receptor ga  
 40 89 6.9 1512 2 T14883 hypothetical prote  
 41 88.5 6.9 119 2 PH1503 ig heavy chain v r  
 42 88.5 6.9 126 2 S40335 ig kappa chain v-j  
 43 88.5 6.9 128 2 A26406 ig kappa chain v r  
 44 88.5 6.9 268 2 A56446 ig heavy chain v r  
 45 88.5 6.9 430 2 I48142 B-lymphocyte anti

## ALIGNMENTS

## RESULT 1

## HLMSP3

poliovirus receptor homolog precursor - mouse  
 C:Species: Mus musculus domesticus (western European house mouse)

C>Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 09-Jul-2004

C:Accession: A38211

R:Morrisson, M.E.; Racaniello, V.R.

J. Virol. 66, 2807-2813, 1992

A:Title: Molecular cloning and expression of a murine homolog of the human poliovirus rec

A:Reference number: A38211; MUID:92219365; PMID:1560525

A:Accession: A38211

A:Molecule type: DNA

A:Residues: 1-467 <MOR>

A:Cross-references: UNIPROT:P32507; UNIPARC:UPI000002B1F6; GB:M80206; NID:g199785; PIDN:f

C:Superfamily: poliovirus receptor; immunoglobulin homology

C:Keywords: duplication; glycoprotein; transmembrane protein

F1-25/Domain: signal sequence #status predicted <Sig>

F126-467/Product: poliovirus receptor homolog #status predicted <MAT>

F126-354/Domain: extracellular #status predicted <EXT>

F147-133/Domain: immunoglobulin homology <IMM1>

F167-231/Domain: immunoglobulin homology <IMM2>

F1267-322/Domain: immunoglobulin homology <IMM3>

F1355-374/Domain: transmembrane #status predicted <TMN>

F1375-467/Domain: intracellular #status predicted <INT>

F154-131,174-229,274-320/Disulfide bonds: #status predicted

F128,138,315/Binding site: carbohydrate (Asn) #status predicted

Query Match 9.5%; Score 122.5; DB 1; Length 467;

Best Local Similarity 26.7%; Pred. No. 0.014;

Matches 46; Conservative 21; Mismatches 56; Indels 49; Gaps 7;

QY 5 LLLIWAQ-----LRQAPLASGMGTGTETTCNISAEGSGSILOCH-LSSTTAQTQYN 58

DB 23 LLLLOETGAQDVRVRLPEVRGLGGTVE-----LPCHLPPPTTERVSQVT 68

QY 59 WEQOQLLAICNADLGWHISPSF-----KDRV-----AFPGGLGLTQSL 98

DB 69 WQRLDGTVA-----FHFSFGVDFPNSQFSKDRLSFVRARPETNADRLDRLAFLRGL 121

QY 99 TVNDTGEVFCIVHTYDPDGTGTGRIFLEVLSVAHGARFQIPILGMAATL 150

DB 122 RVEDEGNTCEPATFPNGTRGVTLRLVI--AQPNHAEAEQVTTGPOQSVAV 171

## RESULT 2

## A53437

poliovirus receptor mPVR - mouse

C:Species: Mus musculus (house mouse)

C>Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C:Accession: A53437

R:Aoki, J.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.

J. Biol. Chem. 269, 8431-8436, 1994

Qy	110	YHTVPDGYTGRIPILEV-----LESSVAEHGARFQIPLIGAMAATLVICTAV-----	157
Db	126	FATPFTGNRESQLNLTWMAKPTNWTIEGTVQVLRAK-----KGDDKVLVATCTSANGKPP	180
Qy	158	IVVVALTRKKEKALRIHSVEGDLRRKSAGQEWSPPAS	194

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 4, 2006, 06:05:59 ; Search time 20 Seconds  
(without alignments)  
244.005 Million cell updates/sec

Title: US-10-658-482-2

Perfect score: 1286

Sequence: 1 MRWCLLIWAQGLRQAPLAS.....YFNVLSYSLGNCSPFTETG 244

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

\*Searched: 135346 seqs, 20000420 residues

Total number of hits satisfying chosen parameters: 135346

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA New.\*
- 1: /cgn2.6/prodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
  - 2: /cgn2.6/prodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
  - 3: /cgn2.6/prodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
  - 4: /cgn2.6/prodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 5: /cgn2.6/prodata/1/pubpaa/US05\_NEW\_PUB.pep.\*
  - 6: /cgn2.6/prodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
  - 7: /cgn2.6/prodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
  - 8: /cgn2.6/prodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	140.5	10.9	555	US-10-821-234-1015	Sequence 1015, Ap
2	106	8.2	7968	US-11-186-731-5	Sequence 5, Appl
3	101	7.9	277	US-11-126-817-54	Sequence 54, Appl
4	99	7.7	406	US-11-000-463-377	Sequence 377, App
5	99	7.7	406	US-11-000-463-849	Sequence 849, App
6	95.5	7.4	215	US-10-131-828A-488	Sequence 488, App
7	95.5	7.4	215	US-10-973-115B-488	Sequence 488, App
8	95.5	7.4	215	US-11-080-991-112	Sequence 112, App
9	94.5	7.3	463	US-10-063-703-86	Sequence 86, Appl
10	94.5	7.3	463	US-11-102-240-86	Sequence 86, Appl
11	93.5	7.3	463	US-11-000-463-872	Sequence 872, App
12	93.5	7.3	567	US-11-000-463-400	Sequence 400, App
13	93	7.2	269	US-10-131-826A-530	Sequence 530, App
14	93	7.2	269	US-10-973-115B-530	Sequence 530, App
15	93	7.2	269	US-11-219-146-2	Sequence 2, Appl
16	93	7.2	686	US-11-072-175-225	Sequence 225, App
17	92.5	7.2	551	US-11-000-463-346	Sequence 346, App
18	91	7.1	247	US-11-084-717-23	Sequence 23, Appl
19	91	7.1	247	US-11-179-244-23	Sequence 23, Appl
20	91	7.1	247	US-11-084-055B-23	Sequence 23, Appl
21	91	7.1	269	US-11-219-146-4	Sequence 4, Appl
22	91	7.1	269	US-11-219-146-6	Sequence 6, Appl
23	91	7.1	269	US-11-219-146-8	Sequence 8, Appl
24	90.5	7.0	199	US-11-219-146-42	Sequence 42, Appl
25	90.5	7.0	199	US-11-219-146-44	Sequence 44, Appl

26	90.5	7.0	209	7	US-11-219-146-18	Sequence 18, Appl
27	90	7.0	107	6	US-10-946-836A-16	Sequence 16, Appl
28	90	7.0	107	6	US-10-988-207-16	Sequence 16, Appl
29	89.5	7.0	508	6	US-10-514-534-7	Sequence 7, Appl
30	89	6.9	247	7	US-11-084-717-25	Sequence 25, Appl
31	89	6.9	247	7	US-11-179-244-25	Sequence 25, Appl
32	89	6.9	247	7	US-11-084-055B-25	Sequence 25, Appl
33	88.5	6.9	139	7	US-11-125-837-24	Sequence 24, Appl
34	88.5	6.9	199	7	US-11-219-146-46	Sequence 46, Appl
35	88.5	6.9	199	7	US-11-219-146-48	Sequence 48, Appl
36	88.5	6.9	209	7	US-11-219-146-20	Sequence 20, Appl
37	88.5	6.9	209	7	US-11-219-146-22	Sequence 22, Appl
38	88.5	6.9	236	7	US-11-086-289-8	Sequence 8, Appl
39	88	6.8	135	6	US-10-993-543-120	Sequence 120, App
40	88	6.8	215	6	US-10-374-954-7	Sequence 7, Appl
41	87.5	6.8	288	6	US-10-821-234-1062	Sequence 1062, Ap
42	87.5	6.8	359	6	US-10-055-877-265	Sequence 265, App
43	87.5	6.8	359	7	US-11-080-091-1	Sequence 1, Appl
44	87.5	6.8	359	7	US-11-116-939-15	Sequence 15, Appl
45	87.5	6.8	359	7	US-11-087-177-23	Sequence 23, Appl

#### ALIGNMENTS

RESULT 1  
US-10-821-234-1015  
; Sequence 1015, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preseclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; PRIOR FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pf\_seq\_genes Version 1.0  
; SEQ ID NO 1015  
; LENGTH: 555  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1015

Query Match 10.9%; Score 140.5; DB 6; Length 555;  
Best Local Similarity 27.3%; Pred. No. 1.3e-05;  
Matches 48; Conservative 24; Mismatches 65; Indels 39; Gaps 6;  
QY 3 WCLLIWAQGLRQAPLASGMMTGTTTGNISAEKGSIILOC-HLSSTTAOTVONWQ 61  
DB 60 WLLLL-----LLASFTGRCPAGELETSVTVVLGDAKLPFCYRGDSGEQGVQVAVAR 114  
QY 62 QD-----QLLAICADNLGWHISPEKDRVAPQ-----GLGLTLQSLTVDNTGEVFCY 110  
DB 115 VDAGAGAEALLHSHKYLHVSYPAYEGRVEQPPPPRPLDGSVLLRNVAQDEGEYCV 174  
QY 111 HTYPTGTYGRIFLEVLSSVAEHGARGFQIPLLGAM-----AATLVVICTA 156  
DB 175 STFPAGSFOARLRVL-----VPLPLNPGPALGEGQLTAAASCTA 218

#### RESULT 2

US-11-186-731-5  
; Sequence 5, Application US/11186731  
; Publication No. US2005025521A1  
; GENERAL INFORMATION:  
; APPLICANT: Kapeller-Libermann, Rosana  
; APPLICANT: Acton, Susan L.  
; TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 4, 2006, 06:04:18 ; Search time 47 Seconds  
(without alignments)  
429.210 Million cell updates/sec

Title: US-10-658-482-2

Perfect score: 1286

Sequence: 1 MWCLLLIWAQGLRQAPLAS.....YFNVLSYSLGNCSPFTTGT 244

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Search: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/1aa/5\_COMB.pep.\*  
2: /cgn2\_6/prodata/1/1aa/6\_COMB.pep.\*  
3: /cgn2\_6/prodata/1/1aa/H\_COMB.pep.\*  
4: /cgn2\_6/prodata/1/1aa/PCUS\_COMB.pep.\*  
5: /cgn2\_6/prodata/1/1aa/RE\_COMB.pep.\*  
6: /cgn2\_6/prodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	9.5	479	2	US-09-723-368-2
2	122	9.5	479	2	US-09-949-016-6278
3	122	9.5	522	2	US-09-949-016-7563
4	111.5	8.7	518	2	US-09-919-172-20
5	107	8.3	514	2	US-09-949-016-11380
6	107	8.3	517	2	US-09-723-368-4
7	106	8.2	458	2	US-09-435-956A-1
8	105	8.2	408	2	US-09-724-864-62
9	104.5	8.1	417	2	US-09-949-016-6729
10	104.5	8.1	456	2	US-09-949-016-7564
11	99.5	7.7	127	1	US-08-137-117D-37
12	99.5	7.7	127	1	US-08-436-717-37
13	98	7.6	128	1	US-08-379-057-12
14	98	7.6	234	2	US-09-740-002-26
15	98	7.6	240	2	US-09-049-672A-11
16	97	7.5	126	1	US-07-634-278-21
17	97	7.5	126	1	US-08-477-728-21
18	97	7.5	126	1	US-08-474-040-21
19	97	7.5	126	1	US-08-487-200-21
20	97	7.5	126	2	US-08-484-537-21
21	97	7.5	129	4	PCT-US95-07372-12
22	96.5	7.5	551	2	US-08-896-537A-2
23	95.5	7.4	215	2	US-09-949-016-6658
24	95.5	7.4	215	2	US-09-991-181-389
25	95.5	7.4	215	2	US-09-990-444-389
26	95.5	7.4	215	2	US-09-997-333-389
27	95.5	7.4	215	2	US-09-992-598-389

28 95.5 7.4 263 2 US-09-949-016-10819 Sequence 10819, A  
29 95.5 7.4 354 2 US-09-393-627B-28 Sequence 28, Appl  
30 95 7.4 544 2 US-09-999-833A-259 Sequence 259, App  
31 95 7.4 544 2 US-10-020-445A-259 Sequence 259, App  
32 95 7.4 1011 1 US-08-162-809-12 Sequence 12, Appl  
33 94.5 7.3 463 2 US-10-012-231A-160 Sequence 160, App  
34 94.5 7.3 463 2 US-10-015-389A-160 Sequence 160, App  
35 94.5 7.3 463 2 US-10-006-768A-160 Sequence 160, App  
36 94.5 7.3 463 2 US-10-015-393A-160 Sequence 160, App  
37 94.5 7.3 463 2 US-10-015-393A-160 Sequence 160, App  
38 94.5 7.3 463 2 US-10-011-833A-160 Sequence 160, App  
39 94.5 7.3 463 2 US-10-006-041A-160 Sequence 160, App  
40 94.5 7.3 463 2 US-10-012-064A-160 Sequence 160, App  
41 94.5 7.3 1138 2 US-09-252-991A-20291 Sequence 20291, A  
42 93.5 7.3 1248 2 US-09-949-016-10595 Sequence 10595, A  
43 93.5 7.3 1248 2 US-09-949-016-10595 Sequence 10595, A  
44 93 7.2 269 2 US-09-430-503-2 Sequence 2, Appli  
45 93 7.2 269 2 US-10-012-231A-364 Sequence 364, App

## ALIGNMENTS

RESULT 1  
US-09-723-368-2  
; Sequence 2, Application US/09723368  
; Patent No. 6641818  
; GENERAL INFORMATION:  
; APPLICANT: NORTHWESTERN UNIVERSITY  
; APPLICANT: SPEAR, Patricia G.  
; APPLICANT: WARNER, Morgyn S.  
; APPLICANT: GERAGHTY, Robert G.  
; APPLICANT: MARTINEZ, Wanda M.  
; APPLICANT: MONTGOMERY, Rebecca I.  
; APPLICANT: COHEN, Gary H.  
; APPLICANT: EISENBERG, Roselyn J.  
; APPLICANT: WHITBECK, Charles J.  
; APPLICANT: KRUMENACHER, Claude  
; APPLICANT: UNIVERSITY OF PENNSYLVANIA  
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY  
; FILE REFERENCE: 200290.0050/2U1  
; CURRENT APPLICATION NUMBER: US/09/723,368  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: U.S. 60/087,862  
; PRIOR FILING DATE: 1998-06-03  
; PRIOR APPLICATION NUMBER: PCT/US99/12235  
; PRIOR FILING DATE: 1999-06-02  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 479  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-723-368-2

Query Match 9.5%; Score 122; DB 2; Length 479;  
Best Local Similarity 25.2%; Pred. No. 0.0013;  
Matches 39; Conservative 21; Mismatches 51; Indels 44; Gaps 6;

QY 3 WCLLLIWAQGLRQAPLASGMGTGTIETGNTSIAEKGGSIILOCHLSSTT--AQVTOVWNE 60  
DB 19 WPLLLLLL-----LETGAQDVRVQVLPEVRGQGGTVELPCHLLPPVPGYISLVTWQ 71  
QY 61 QOD-----QLLAICNADLGMHISPSFKORVAPGPG-----LG 92  
DB 72 RPDAPANNQVNAFPRKMG-----PSFP---SPKPSGRSLFSVSAKQSTQDTEAELODAT 124  
QY 93 LTQLSLTYNDTGEYFCIYHTYTDGTYTGRIFLEVL 127  
DB 125 LALHGLITVEDEGNYTCFATPPKGSVRGWTWLRVI 159

RESULT 2

US-09-949-016-6278  
; Sequence 6278, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6278  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6278

Query Match 9.5%; Score 122; DB 2; Length 479;  
Best Local Similarity 25.2%; Pred. No. 0.0013;  
Matches 39; Conservative 21; Mismatches 51; Indels 44; Gaps 6;

QY 3 WCLLLIWAQGLRQAPLASGNMTGTTGNISAEKGSIILOCHLSST--AOVTQVNW 60  
DB 19 WPLLIIWAQGLRQAPLASGNMTGTTGNISAEKGSIILOCHLSST--AOVTQVNW 60  
QY 61 QOD-----QLLAIACNADLGNHISPSFKDVRVAPGP-----LG 92  
DB 72 RPDAPANHONVAAPFKPMG-----PSPF---SPKPSERLSFVSAKOSTGQDTEAELODAT 124  
QY 93 LTQLSILVNDTGEYFCIYHTYDPDGTGTGRIFLEV 127  
DB 125 LALHGLTVEDEGNYTCEPATFPKGSVRGWTWLRVI 159

RESULT 3  
US-09-949-016-7563  
; Sequence 7563, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7563  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-7563

Query Match 9.5%; Score 122; DB 2; Length 522;  
Best Local Similarity 25.2%; Pred. No. 0.0015;  
Matches 39; Conservative 21; Mismatches 51; Indels 44; Gaps 6;

QY 3 WCLLLIWAQGLRQAPLASGNMTGTTGNISAEKGSIILOCHLSST--AOVTQVNW 60  
DB 62 WPLLIIWAQGLRQAPLASGNMTGTTGNISAEKGSIILOCHLSST--AOVTQVNW 114

QY 61 QOD-----QLLAIACNADLGNHISPSFKDVRVAPGP-----LG 92  
DB 115 RPDAPANHONVAAPFKPMG-----PSPF---SPKPSERLSFVSAKOSTGQDTEAELODAT 167  
QY 93 LTQLSILVNDTGEYFCIYHTYDPDGTGTGRIFLEV 127  
DB 168 LALHGLTVEDEGNYTCEPATFPKGSVRGWTWLRVI 202

RESULT 4  
US-09-919-172-20  
; Sequence 20, Application US/09919172  
; Patent No. 6673545  
; GENERAL INFORMATION:  
; APPLICANT: Faris, Mary  
; APPLICANT: Turner, Christopher M.  
; TITLE OF INVENTION: PROSTATE CANCER MARKERS  
; FILE REFERENCE: PA-0036 US  
; CURRENT APPLICATION NUMBER: US/09/919,172  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/222,469  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PERL Program  
; SEQ ID NO 20  
; LENGTH: 518  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6673545 3189059CD1  
US-09-919-172-20

Query Match 8.7%; Score 111.5; DB 2; Length 518;  
Best Local Similarity 24.4%; Pred. No. 0.016;  
Matches 53; Conservative 33; Mismatches 84; Indels 47; Gaps 11;

QY 2 RWCLLIW--AQLROAPLASGNMTGTTGNISAEKGSIILOCHLS--TTAQTQV 57  
DB 12 RW-----WGLALGL-TAFFLPVHVSQVQVNDMSMYGFTGTVVLRHCSFANPLPSVKITQV 65  
QY 58 NWEQ-----QDLIAICNADLGNHISPSFKDRV---APGPGLG-LTLQSLTVNDTGYFCI 109  
DB 66 TWOKSTNGSKQNVAIYVPSMGVSLAPYRVEFLPSTGDTGIRLSRLEDEGVYICE 125  
QY 110 YHTYDPGTGTGRIFLEV-----LESSVAEHGARFQIPLLGAMAATLVVICTAV----- 157  
DB 126 FATFPTGNRESQLNTVMKPTNWIETQAVLRK-----KGQDDKVLVATCTTSANGKPP 180  
QY 158 IVVVALTRKKALRIHSVGDLRKKSAGQEWSPSAP 194  
DB 181 SVVSWETRLKGEARVPGDSG-----TPMAP 205

RESULT 5  
US-09-949-016-11380  
; Sequence 11380, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012

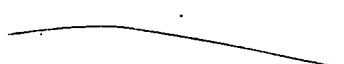


November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rnpbm** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New).  
Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).



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## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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